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| (54) Title: NUCLEIC ACID ARRAYS (57) Abstract <p>Arrays of polynucleotide spots and kits comprising the same, as well as methods for their preparation and use are provided. The subject arrays include a plurality of polynucleotide spots stably associated with the surface of a solid support. At least a portion of the polynucleotide spots comprises a polynucleotide probe composition that is made up of unique polynucleotides, where all of the unique polynucleotides of the array correspond to a common type of gene. Also provided are sets of a representational number of gene specific primers suitable for use in generating target nucleic acid for use with the subject arrays. The subject arrays find use in hybridization assays, particularly in assays for the identification of differential gene expression patterns among two or more different types of cells.</p> | | |

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NUCLEIC ACID ARRAYS

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuation-in-part of application serial no. 08/859,998 filed on
5 May 21, 1997 and application serial no. 09/053,375 filed on March 31, 1998, the disclosures
of which are herein incorporated by reference.

INTRODUCTION

Technical Field

10 The field of this invention is biopolymeric arrays.

Background of the Invention

“Biochips” or arrays of binding agents, such as oligonucleotides and peptides, have
become an increasingly important tool in the biotechnology industry and related fields.
15 These binding agent arrays, in which a plurality of binding agents are deposited onto a solid
support surface in the form of an array or pattern, find use in a variety of applications,
including drug screening, nucleic acid sequencing, mutation analysis, and the like. One
important use of biochips is in the analysis of differential gene expression, where the
expression of genes in different cells, normally a cell of interest and a control, is compared
20 and any discrepancies in expression are identified. In such assays, the presence of
discrepancies indicates a difference in the classes of genes expressed in the cells being
compared.

In methods of differential gene expression, arrays find use by serving as a substrate to
which is bound polynucleotide “probe” fragments. One then obtains “targets” from

analogous cells, tissues or organs of a healthy and diseased organism. The targets are then hybridized to the immobilized set of polynucleotide "probe" fragments. Differences between the resultant hybridization patterns are then detected and related to differences in gene expression in the two sources.

5 A variety of different array technologies have been developed in order to meet the growing need of the biotechnology industry, as evidenced by the extensive number of patents and references listed in the relevant literature section below.

 Despite the wide variety of array technologies currently in preparation or available on the market, there is a continued need to identify new array devices to meet the needs of
10 specific applications. Of particular interest would be the development of an array capable of providing high throughput analysis of differential gene expression.

Relevant Literature

 Patents and patent applications describing arrays of biopolymeric compounds and
15 methods for their fabrication include: 5,242,974; 5,384,261; 5,405,783; 5,412,087; 5,424,186; 5,429,807; 5,436,327; 5,445,934; 5,472,672; 5,527,681; 5,529,756; 5,545,531; 5,554,501; 5,556,752; 5,561,071; 5,599,895; 5,624,711; 5,639,603; 5,658,734; WO 93/17126; WO 95/11995; WO 95/35505; EP 742 287; and EP 799 897.

 Patents and patent application describing methods of using arrays in various
20 applications include: 5,143,854; 5,288,644; 5,324,633; 5,432,049; 5,470,710; 5,492,806; 5,503,980; 5,510,270; 5,525,464; 5,547,839; 5,580,732; 5,661,028; WO 95/21265; WO 96/31622; WO 97/10365; WO 97/27317; EP 373 203; and EP 785 280.

 Other references of interest include: Atlas Human cDNA Expression Array I (April 1997) CLONTECHniques XII: 4-7; Lockhart et al., Nature Biotechnology (1996) 14: 1675-
25 1680; Shena et al., Science (1995) 270: 467-470; Schena et al., Proc. Nat'l Acad. Sci. USA (1996)93:10614-10619; Shalon et al., Genome Res. (1996) 6: 639-645; Milosavljevic et al., Genome Res. (1996) 6:132-141; Nguyen et al., Genomics (1995)29: 207-216; Piétu et al., Genome Res. (1996) 6: 492-503; Zhao et al., Gene (1995) 166:207-213; Chalifour et al., Anal. Biochem. (1994) 216:299-304; Heller et al., Proc. Nat'l Acad. Sci. USA (1997) 94:
30 2150-2155; and Schena, M., BioAssays (1996) 18: 427-431.

SUMMARY OF THE INVENTION

Arrays of polynucleotide spots stably associated with the surface of a solid support and kits comprising the same, as well as methods for their preparation and use in hybridization assays, are provided. The subject arrays comprise a plurality of polynucleotide spots, wherein each different polynucleotide spot is made up of a polynucleotide probe composition and at least a portion of the polynucleotide probe compositions are made up of unique polynucleotides. The arrays are further characterized in that all of the unique polynucleotides on the array correspond to the same type of gene. The subject arrays find particular use in differential gene expression analysis. Also provided are sets of a representational number of gene specific primers useful in generating target nucleic acids for use with the subject arrays in hybridization assays.

BRIEF DESCRIPTION OF THE FIGURES

Fig. 1 provides a representation of an array according to the subject invention.

DEFINITIONS

The term "nucleic acid" as used herein means a polymer composed of nucleotides, e.g. deoxyribonucleotides or ribonucleotides.

The terms "ribonucleic acid" and "RNA" as used herein mean a polymer composed of ribonucleotides.

The terms "deoxyribonucleic acid" and "DNA" as used herein mean a polymer composed of deoxyribonucleotides.

The term "oligonucleotide" as used herein denotes single stranded nucleotide multimers of from about 10 to 100 nucleotides in length.

The term "polynucleotide" as used herein refers to single or double stranded polymer composed of nucleotide monomers of greater than about 120 nucleotides in length up to about 1000 nucleotides in length.

The term "array type" refers to the type of gene represented on the array by the unique polynucleotides, where the type of gene that is represented on the array is dependent on the intended purpose of the array, e.g. to monitor expression of key human genes, to monitor expression of known oncogenes, etc, i.e. the use for which the array is designed. As such, all of the unique polynucleotides on a given array correspond to the same type or

category or group of genes. Genes are considered to be of the same type if they share some common linking characteristics, such as: species of origin, e.g. human, mouse, rat, etc.; tissue or cell type of origin, e.g. muscle, neural, dermal, organ, etc.; disease state, e.g. cancer; functions, e.g. protein kinases, tumor suppressors and the like, participation in the same
5 normal biological process, e.g. apoptosis, signal transduction, cell cycle regulation, proliferation, differentiation etc.; and the like. For example, one array type that is provided below is a "cancer array" in which each of the "unique" polynucleotide probes correspond to a gene associated with a cancer disease state. Likewise, a "human array" may be an array of polynucleotides corresponding to unique tightly regulated human genes. Similarly, an
10 "apoptosis array" may be an array type in which the polynucleotides correspond to unique genes associated with apoptosis.

The "unique" polynucleotide sequences associated with each type of array of the present invention are sequences which are distinctive or different with respect to every other polynucleotide sequence on the array and correspond to the same type of gene, as defined
15 above. For example, in a cancer array, each unique polynucleotide has a sequence that is not homologous to any other known cancer associated sequence. Moreover, each polynucleotide sequence on the array is statistically chosen to ensure that the probability of homology to any sequence of that type is very low. Moreover, in the cancer array embodiment, all sequences are statistically chosen to insure that the probability of homology to any other sequence
20 associated with cancer or of human origin is very low. An important feature of the individual polynucleotide probe compositions of the subject arrays is that they are only a fragment of the entire cDNA of the gene to which they correspond. In other words, for each gene represented on the array, the entire cDNA sequence the gene is not represented on the array. Instead, the sequence of only a portion or fragment of the entire cDNA is represented on the
25 array by this unique polynucleotide.

The term "polynucleotide probe composition" refers to the nucleic acid composition that makes up each of the spots on the array. Thus, the term "polynucleotide probe composition" includes nucleic acid compositions of unique polynucleotides and control or calibrating polynucleotides (e.g. polynucleotides corresponding to housekeeping genes). The
30 polynucleotide compositions are made up of single stranded polynucleotides (i.e. polynucleotides that are not hybridized to each other), where all of the polynucleotides in the probe composition may be identical to each other or there may be two different

polynucleotides (polynucleotides of different nucleotide sequence) in each probe composition, where the two different polynucleotides are complementary to each other.

The term "gene specific primer" means a polynucleotide of sufficient length to specifically hybridize to a distinct nucleic acid member of the sample, *e.g.* RNA or cDNA, where the length of the gene specific primers will usually be at least 8 nt, more usually at least 20 nt and may be as long as 25 nt or longer, but will usually not exceed 50 nt. The gene specific primers of the subject invention are sufficiently specific to hybridize to complementary template sequence during the generation of labeled nucleic acids under conditions sufficient for first strand cDNA synthesis, which conditions are known by those of skill in the art. The number of mismatches between the gene specific primer sequences and their complementary template sequences to which they hybridize during the generation of labeled nucleic acids in the subject methods will generally not exceed 20 %, usually will not exceed 10 % and more usually will not exceed 5 %, as determined using the FASTA program using default settings.

DESCRIPTION OF THE SPECIFIC EMBODIMENTS

Arrays of polynucleotide spots and methods for their preparation are provided. In the subject arrays, a plurality of polynucleotide spots is stably associated with the surface of a solid support, where at least a portion of the polynucleotide spots on the array are made up of unique polynucleotides and all of the unique polynucleotides of the array correspond to one particular type of gene, *e.g.* tightly regulated human genes, genes associated with a particular disease state, genes associated with cell cycle regulation, etc. The subject arrays find particular use in gene expression assays. Also provided are sets of a representational number of gene specific primers useful in generating target nucleic acids for use with the subject arrays. In further describing the subject invention, the arrays first will be described in general terms. Next, methods for their preparation are described. Following this, a description of representative specific array types falling within the scope of the invention will be provided. Finally, a review of representative applications in which the subject arrays may be employed will be provided, where this review includes a description of the sets of a representational number of gene specific primers according to the subject invention.

Before the subject invention is further described, it is to be understood that the invention is not limited to the particular embodiments of the invention described below, as variations of the particular embodiments may be made and still fall within the scope of the appended claims. It is also to be understood that the terminology employed is for the purpose
5 of describing particular embodiments, and is not intended to be limiting. Instead, the scope of the present invention will be established by the appended claims.

In this specification and the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Unless defined
10 otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs.

ARRAYS OF THE SUBJECT INVENTION-GENERAL DESCRIPTION

15 *Array Structure*

The arrays of the subject invention have a plurality of polynucleotide spots stably associated with a surface of a solid support. Each spot on the array comprises a polynucleotide sample, i.e. polynucleotide probe composition, of known identity, usually of known sequence, as described in greater detail below. The polynucleotide spots on the array
20 may be any convenient shape, but will typically be circular, ellipsoid, oval or some other analogously curved shape. The density of the spots on the solid surface is at least about $5/\text{cm}^2$ and usually at least about $10/\text{cm}^2$ but does not exceed about $1000/\text{cm}^2$, and usually does not exceed about $500/\text{cm}^2$, and more usually does not exceed about $300/\text{cm}^2$. The spots may be arranged in any convenient pattern across or over the surface of the array, such as in
25 rows and columns so as to form a grid, in a circular pattern, and the like, where generally the pattern of spots will be present in the form of a grid across the surface of the solid support. See Fig. 1.

In the subject arrays, the spots of the pattern are stably associated with the surface of a solid support, where the support may be a flexible or rigid solid support. By stably
30 associated is meant that the polynucleotides of the spots maintain their position relative to the solid support under hybridization and washing conditions. As such, the polynucleotide members which make up the spots can be non-covalently or covalently stably associated

with the support surface. Examples of non-covalent association include non-specific adsorption, binding based on electrostatic (e.g. ion, ion pair interactions), hydrophobic interactions, hydrogen bonding interactions, specific binding through a specific binding pair member covalently attached to the support surface, and the like. Examples of covalent binding include covalent bonds formed between the spot polynucleotides and a functional group present on the surface of the rigid support, e.g. -OH, where the functional group may be naturally occurring or present as a member of an introduced linking group, as described in greater detail below.

As mentioned above, the array is present on either a flexible or rigid substrate. By flexible is meant that the support is capable of being bent, folded or similarly manipulated without breakage. Examples of solid materials which are flexible solid supports with respect to the present invention include membranes, e.g. nylon, flexible plastic films, and the like. By rigid is meant that the support is solid and does not readily bend, i.e. the support is not flexible. As such, the rigid substrates of the subject arrays are sufficient to provide physical support and structure to the polymeric targets present thereon under the assay conditions in which the array is employed, particularly under high throughput handling conditions. Furthermore, when the rigid supports of the subject invention are bent, they are prone to breakage.

The solid supports upon which the subject patterns of spots are presented in the subject arrays may take a variety of configurations ranging from simple to complex, depending on the intended use of the array. Thus, the substrate could have an overall slide or plate configuration, such as a rectangular or disc configuration. In many embodiments, the substrate will have a rectangular cross-sectional shape, having a length of from about 10 mm to 200 mm, usually from about 40 to 150 mm and more usually from about 75 to 125 mm and a width of from about 10 mm to 200 mm, usually from about 20 mm to 120 mm and more usually from about 25 to 80 mm, and a thickness of from about 0.01 mm to 5.0 mm, usually from about 0.1 mm to 2 mm and more usually from about 0.2 to 1 mm.

The substrates of the subject arrays may be fabricated from a variety of materials. The materials from which the substrate is fabricated should ideally exhibit a low level of non-specific binding during hybridization events. In many situations, it will also be preferable to employ a material that is transparent to visible and/or UV light. For flexible substrates, materials of interest include: nylon, both modified and unmodified, nitrocellulose.

polypropylene, and the like, where a nylon membrane, as well as derivatives thereof, is of particular interest in this embodiment. For rigid substrates, specific materials of interest include: glass; plastics, e.g. polytetrafluoroethylene, polypropylene, polystyrene, polycarbonate, and blends thereof, and the like; metals, e.g. gold, platinum, and the like; etc.

5 The substrates of the subject arrays comprise at least one surface on which the pattern of spots is present, where the surface may be smooth or substantially planar, or have irregularities, such as depressions or elevations. The surface on which the pattern of spots is present may be modified with one or more different layers of compounds that serve to modify the properties of the surface in a desirable manner. Such modification layers, when
10 present, will generally range in thickness from a monomolecular thickness to about 1 mm, usually from a monomolecular thickness to about 0.1 mm and more usually from a monomolecular thickness to about 0.001 mm. Modification layers of interest include: inorganic and organic layers such as metals, metal oxides, polymers, small organic molecules and the like. Polymeric layers of interest include layers of: peptides, proteins,
15 polynucleic acids or mimetics thereof, e.g. peptide nucleic acids and the like; polysaccharides, phospholipids, polyurethanes, polyesters, polycarbonates, polyureas, polyamides, polyethyleneamines, polyarylene sulfides, polysiloxanes, polyimides, polyacetates, and the like, where the polymers may be hetero- or homopolymeric, and may or may not have separate functional moieties attached thereto, e.g. conjugated.

20 The total number of spots on the substrate will vary depending on the number of different polynucleotide probes one wishes to display on the surface, as well as the number of control spots, calibrating spots and the like, as may be desired depending on the particular application in which the subject arrays are to be employed. Generally, the pattern present on the surface of the array will comprise at least about 10 distinct spots, usually at least about
25 20 distinct spots, and more usually at least about 50 distinct spots, where the number of spots may be as high as 10,000 or higher, but will usually not exceed about 5,000 distinct spots, and more usually will not exceed about 3,000 distinct spots. In many embodiments, it is preferable to have each distinct probe composition presented in duplicate, i.e. so that there are two spots for each distinct polynucleotide probe composition of the array. In certain
30 embodiments, the number of spots will range from about 200 to 600.

 The amount of polynucleotide present in each spot will be sufficient to provide for adequate hybridization and detection of target nucleic acid during the assay in which the

array is employed. Generally, the amount of polynucleotide in each spot will be at least about 0.1 ng, usually at least about 0.5 ng and more usually at least about 1 ng, where the amount may be as high as 1000 ng or higher, but will usually not exceed about 20 ng and more usually will not exceed about 10 ng. The copy number of each polynucleotide in a spot
5 will be sufficient to provide enough hybridization sites for target molecule to yield a detectable signal, and will generally range from about 0.01 fmol to 50 fmol, usually from about 0.05 fmol to 20 fmol and more usually from about 0.1 fmol to 5 fmol. Where the spot has an overall circular dimension, the diameter of the spot will generally range from about 10 to 5,000 μm , usually from about 20 to 2,000 μm and more usually from about 50 to 1000
10 μm .

A critical feature of the subject arrays is that at least a portion, usually the majority, of the polynucleotide spots on the array are made up of polynucleotide probes that all correspond to the same kind or kind of gene, i.e. genes that all share some common characteristic or can be grouped together based on some common feature, such as species of
15 origin, tissue or cell of origin, functional role, disease association, etc. Other spots which may be present in the pattern include spots comprising genomic DNA, housekeeping genes, negative and positive control genes, and the like. These latter types of spots comprise polynucleotides that are not "unique" as that term is defined and used herein, i.e. they are "common." In other words, they are calibrating or control genes whose function is not to tell
20 whether a particular "key" gene of interest is expressed, but rather to provide other useful information, such as background or basal level of expression, and the like. The percentage of spots which are made of unique polynucleotides that correspond to the same type of gene is generally at least about 30 number %, and usually at least about 60 number % and more usually at least about 80 number %. Therefore, the arrays of the subject invention will be of a
25 specific array type, where representative array types include: human arrays, mouse arrays, cancer arrays, apoptosis arrays, human stress arrays, oncogene and tumor suppressor arrays, cell-cell interaction arrays, cytokine and cytokine receptor arrays, rat arrays, blood arrays, mouse stress arrays, neuroarrays, and the like, where some of these representative arrays are described in greater detail below.

30 With respect to the polynucleotide probes that correspond to a particular type or kind of gene, type or kind can refer to a plurality of different characterizing features, where such features include: species specific genes, where specific species of interest include eukaryotic

species, such as mice, rats, rabbits, pigs, primates, humans, etc.; function specific genes, where such genes include oncogenes, apoptosis genes, cytokines, receptors, protein kinases, etc.; genes specific for or involved in a particular biological process, such as apoptosis, differentiation, cell cycle regulation, cancer, aging, proliferation, etc.; location specific
5 genes, where locations include organ, such as heart, liver, prostate, lung etc., tissue, such as nerve, muscle, connective, etc., cellular, such as axonal, lymphocytic, etc, or subcellular locations, e.g. nucleus, endoplasmic reticulum, Golgi complex, endosome, lysosome, peroxisome, mitochondria, cytoplasm, cytoskeleton, plasma membrane, extracellular space; specific genes that change expression level over time, e.g. genes that are expressed at
10 different levels during the progression of a disease condition, such as prostate genes which are induced or repressed during the progression of prostate cancer.

The average length of the polynucleotides on the array is chosen to be of sufficient length to provide a strong and reproducible signal, as well as tight and robust hybridization. As such, the average length of the polynucleotides of the array will typically range from
15 about 120 to 1000 nt and usually from about 120 to 800 nt, where in many embodiments, the average length ranges from about 200 to 700 nt, and usually 200 to 600 nt. The length of each polynucleotide on the array is less than the length of the mRNA to which it corresponds. As such, the polynucleotide represents only a fraction of the full length cDNA to which it corresponds.

20 As mentioned above, the subject arrays typically comprise one or more additional spots of polynucleotides which do not correspond to the array type, i.e. the type or kind of gene represented on the array. In other words, the array may comprise one or more spots that are made of non "unique" polynucleotides, i.e common polynucleotides. For example, spots comprising genomic DNA may be provided in the array, where such spots may serve as
25 orientation marks. Spots comprising plasmid and bacteriophage genes, genes from the same or another species which are not expressed and do not cross hybridize with the cDNA target, and the like, may be present and serve as negative controls. In addition, spots comprising housekeeping genes and other control genes from the same or another species may be present, which spots serve in the normalization of mRNA abundance and standardization of
30 hybridization signal intensity in the sample assayed with the array.

Polynucleotide Probes of the Arrays

Each spot of the pattern present on the surface of the substrate is made up of a unique polynucleotide probe composition. By "polynucleotide probe composition" is meant a collection or population of single stranded polynucleotides capable of participating in a hybridization event under appropriate hybridization conditions, where each of the individual polynucleotides may be the same -- have the same nucleotide sequence-- or different sequences, for example the probe composition may consist of 2 different single stranded polynucleotides that are complementary to each other (i.e. the two different polynucleotides in the spot are complementary but physically separated so as to be single stranded, i.e. not hybridized to each other). In many embodiments, the probe compositions will comprise two complementary, single stranded polynucleotides.

In those polynucleotide probe compositions having unique polynucleotides, the sequence of the polynucleotides are chosen in view of the type and the intended use of the array on which they are present. The unique polynucleotides are chosen so that each distinct unique polynucleotide does not cross-hybridize with any other distinct unique polynucleotide on the array, i.e. the polynucleotide of any other polynucleotide probe composition that corresponds to a different gene falling within the broad category or type of genes represented on the array. As such, the nucleotide sequence of each unique polynucleotide of a probe composition will have less than 90% homology, usually less than 85 % homology, and more usually less than 80% homology with any other different polynucleotide of a probe composition of the array, where homology is determined by sequence analysis comparison using the FASTA program using default settings. The sequence of unique polynucleotides in the probe compositions are not conserved sequences found in a number of different genes (at least two), where a conserved sequence is defined as a stretch of from about 40 to 200 nucleotides which have at least about 90% sequence identity, where sequence identity is measured as above. The polynucleotide will generally be a deoxyribonucleic acid having a length of from about 120 to 1000, usually from 120 to 700 nt, and more usually 200 to 600 nt. The polynucleotide will not cross-hybridize with any other polynucleotide on the array under standard hybridization conditions. Again, the length of the polynucleotide will be shorter than the mRNA to which it corresponds.

Array Preparation

The subject arrays can be prepared using any convenient means. One means of preparing the subject arrays is to first synthesize the polynucleotides for each spot and then deposit the polynucleotides as a spot on the support surface. The polynucleotides may be prepared using any convenient methodology, such as automated solid phase synthesis protocols, preparative PCR and like, where preparative PCR or enzymatic synthesis is preferred in view of the length and the large number of polynucleotides that must be generated for each array.

For preparative PCR, primers flanking either side of the portion of the gene of interest will be employed to produce amplified copy numbers of the portion of interest. Methods of performing preparative PCR are well known in the art, as summarized in PCR, Essential Techniques (Ed. J.F. Burke, John Wiley & Sons)(1996). Alternatively, if a gene fragment of interest is cloned into a vector, vector primers can be used to amplify the gene fragment of interest to produce the polynucleotide.

In determining the portion of the gene to be amplified and subsequently placed on the array, regions of the gene having a sequence unique to that gene should preferably be amplified. Different methods may be employed to choose the specific region of the gene to be amplified. Thus, one can use a random approach based on availability of a gene of interest. However, instead of using a random approach which is based on availability of a gene of interest, a rational design approach may also be employed to choose the optimal sequence for the hybridization array. Preferably, the region of the gene that is selected and amplified is chosen based on the following criteria. First, the sequence that is chosen should yield a polynucleotide that does not cross-hybridize with any other polynucleotide that is present on the array. Second, the sequence should be chosen such that the polynucleotide has a low probability of cross-hybridizing with a polynucleotide having a nucleotide sequence found in any other gene, whether or not the gene is to be represented on the array from the same species of origin, e.g. for a human array, the sequence will not be homologous to any other human genes. As such, sequences that are avoided include those found in: highly expressed gene products, structural RNAs, repeated sequences found in the sample to be tested with the array and sequences found in vectors. A further consideration is to select sequences which provide for minimal or no secondary structure, structure which allows for

optimal hybridization but low non-specific binding, equal or similar thermal stabilities, and optimal hybridization characteristics.

The prepared polynucleotides may be spotted on the support using any convenient methodology, including manual techniques, e.g. by micro pipette, ink jet, pins, etc., and automated protocols. Of particular interest is the use of an automated spotting device, such as the Beckman Biomek 2000 (Beckman Instruments). As mentioned above, the polynucleotide probe compositions that are spotted onto the array surface are made up of single stranded polynucleotides, where all the polynucleotides may be identical to each other or a population of complementary polynucleotides may be present in each spot.

10

SPECIFIC ARRAY TYPES OF THE SUBJECT INVENTION

A variety of specific array types are also provided by the subject invention. As discussed above, array type refers to the nature of the polynucleotide probes present on the array and the types of genes to which the probes correspond. These array types include: human array; mouse array; cancer array, apoptosis array, human stress array, oncogene and tumor suppressor array, cell-cell interaction array, and cytokine and cytokine receptor array, as well as other types of arrays, e.g. rat array, rat stress array, blood array, mouse stress array, and nueroarray. Each of these arrays is described separately below.

20

Human Array

One specific array type provided by the subject invention is the human array. In the human array of the subject invention, the majority of the spots on the array have a polynucleotide sequence corresponding to a human gene of interest. As such, all of the unique polynucleotide probes on the array correspond to human genes. The human genes represented on the human array are typically those genes that have been identified by those of skill in the art as key genes. By "key" is meant that the genes are relevant and related to the purpose of the array, e.g. the identification of difference in the expression profiles of different cell or tissue types, where the key genes are generally functionally important to the cell. In many embodiments, the genes represented on the human array are tightly regulated human genes. The term "tightly regulated gene" is used herein in accordance with its art accepted definition and use. As such, by tightly regulated human gene is meant a gene which

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is not "leaky," as opposed to housekeeping genes which are generally expressed at similar levels in different cells and different tissues, i.e. a gene which is inducible such that in response to a specific inducing signal the gene turns "on" and when this signal is removed, the gene turns "off."

5 In certain embodiments of the human array, human genes that may be represented on the subject arrays include: (a) oncogenes & tumor suppressors; (b) cell cycle regulators; (c) stress response proteins; (d) ion channel & transport proteins; (e) intracellular signal transduction modulators and effectors; (f) apoptosis-related proteins; (g) DNA synthesis, repair and recombination proteins; (h) transcription factors & general DNA binding proteins; 10 (i) growth factor & chemokine receptors; (j) interleukin & interferon receptors; (k) hormone receptors; (l) neurotransmitter receptors; (m) cell surface antigens & cell adhesion proteins; (n) growth factors, cytokines and chemokines; (o) interleukins & interferons; (p) hormones; (q) extracellular matrix proteins; (r) cytoskeleton & motility proteins; (s) RNA processing & turnover proteins; (t) post-translational modification, trafficking & targeting proteins; (u) 15 protein turnover; and (v) metabolic pathway proteins.

 In view of the length of the polynucleotides of the probe compositions of the spots, each polynucleotide of a probe composition typically has a nucleotide sequence of only a portion of the human gene. Specific sequences to which the polynucleotide sequence may correspond include those identified in Table 1 below, where by "correspond" is meant that 20 the polynucleotide could have the same sequence as specified or a sequence complementary to the specified sequence. Whether the polynucleotide sequence is the same as a portion of the sense strand of the gene to which it corresponds or complementary thereto is based primarily on the nature of the target which the array is to be used, e.g. if the target is first strand cDNA, the polynucleotide will have a sequence found in the anti-sense DNA strand of 25 the gene to which it corresponds.

 Of particular interest is a human array of the subject invention as shown in Fig. 1. In the array, each spot on the array comprises a known polynucleotide, as specified in Table 1, where the array comprises spots which: (a) correspond to 588 different tightly regulated human genes; (b) comprise plasmid and bacteriophage polynucleotides; (c) comprise 30 polynucleotides corresponding to housekeeping genes; and (d) genomic DNA. Each of the different types of polynucleotide spots are positioned at a known location on the membrane surface.

TABLE I

| Array Coordinate | GeneBank # | Gene Name | Position |
|------------------|------------------------|---|-----------|
| E2i | M29696 | interleukin-7 receptor (IL-7) | 1410-1625 |
| F5i | X01992, M29383 | HUJFN-gamma interferon | 391-586 |
| F5j | J04156 | interleukin 7 (IL-7) | 174-447 |
| A1a | V00568 | c-myc oncogene | 1372-1594 |
| E2m | X01057, X01058, X01402 | interleukin-2 receptor | 1990-2247 |
| F5k | A14844 | interleukin-2 (IL-2) | 181-436 |
| E1a | M29366 | epidermal growth factor receptor (ERBB3) | 3886-4139 |
| C1a | X04434, M24599 | insulin-like growth factor I receptor | 3414-3904 |
| F1a | M29645 | insulin-like growth factor II | 436-618 |
| C1b | L09210 | homo sapiens inducible nitric oxide synthase | 3503-3856 |
| E4f | M64752 | glutamate receptor subunit (GLUH1) | 2232-2567 |
| A1b | X03663 | c-fms proto-oncogene | 2568-2880 |
| C1c | M32315 | tumor necrosis factor receptor | 3359-3543 |
| C1d | Z12020 | p53-associated gene | 920-1232 |
| F1b | X02811 | platelet-derived growth factor B chain | 1663-2125 |
| B1d | X01060 | transferrin receptor | 4382-4770 |
| F5l | X02851 | interleukin-1 precursor (PRE IL-1) | 1107-1473 |
| F5m | K02770 | monocyte interleukin 1 (IL-1) | 917-1208 |
| F5n | M14743 | interleukin 3 (IL-3) | 390-608 |
| F6a | M13982 | interleukin 4 (IL-4) | 216-459 |
| F6b | X04602 | interleukin BSF-2 (B-cell differentiation factor) | 130-555 |
| C1e | X01394 | tumor necrosis factor | 607-879 |
| C1f | D12614 | lymphotoxin (TNF-BETA) | 305-499 |
| E5c | M12807 | T-cell surface glycoprotein T4 | 947-1140 |
| E2n | M20566, X12830 | interleukin 6 receptor | 2359-2823 |
| F6c | X04688 | T-cell replacing factor (interleukin-5) | 35-279 |
| F6d | M28622 | interferon beta-1 (IFN-beta-1) | 345-730 |
| F1c | M11220 | granulocyte-macrophage colony stimulating factor | 121-621 |
| F1d | K03222 | transforming growth factor-alpha | 338-595 |
| F6e | J00209 | leukocyte interferon (IFN-alpha) alpha-C | 89-430 |
| F1e | X02812, J05114 | transforming growth factor-beta (TGF-beta) | 2398-2575 |
| F1f | X03438 | granulocyte colony-stimulating factor (G-CSF) | 901-1232 |
| D1a | M58603 | nuclear factor kappa-B DNA binding subunit | 2544-3019 |
| A1c | M15024 | nucleotide sequence of the c-myc cDNA clone lambda-LMC8 | 1981-2176 |
| C1g | M14694 | p53 cellular tumor antigen | 690-964 |
| F1g | M19154, M22045, M22046 | transforming growth factor beta-2 | 1538-1878 |

TABLE I (CONT)

| Array Coordinate | GeneBank # | Gene Name | Position |
|------------------|------------------------|--|-----------|
| F1h | X04571 | kidney epidermal growth factor (EGF) precursor | 4164-4434 |
| E3a | J03171 | interferon alpha receptor (HUIFN-ALPHA-REC) | 2562-2740 |
| F6f | M57627 | interleukin 10 (IL10) | 442-648 |
| E3b | M26062 | interleukin 2 receptor beta chain (P70-75) | 3399-3748 |
| E3c | M74782 | interleukin 3 receptor (HIL-3RA) | 651-1116 |
| E3d | X52425 | interleukin 4 receptor | 2641-2974 |
| E3e | M75914 | interleukin 5 receptor alpha | 555-959 |
| E3f | X77722 | interferon alpha/beta receptor | 553-1012 |
| F1i | HG1621 | cytokine humig | 2021-2246 |
| E4g | HG1160, M37981 | cholinergic receptor nicotinic alfa polipeptide 3 | 934-1250 |
| E3g | HG1252, D11086 | interleukin 2 receptor gamma polipeptide | 674-1006 |
| E4b | HG1334, M20132, J03180 | androgen receptor | 1879-2146 |
| E1b | HG135, M73238 | ciliary neurotropic factor receptor | 610-849 |
| C1h | HG1410, X68486 | adenosine receptor | 1281-1494 |
| E3h | HG1757, J03143 | interferon gamma receptor | 610-824 |
| E1c | HG2246, M60459 | erythropoietin receptor | 1423-1740 |
| C1i | S56143 | A1 adenosine receptor-adenylate cyclase inhibitor | 508-921 |
| B1e | HG3354, Z30425 | orphan hormone nuclear receptor | 817-1147 |
| C1j | HG3381, X76981 | adenosine receptor A3 | 1043-1452 |
| E4c | L00587 | calcitonin receptor | 885-1270 |
| B1f | HG74, M62424 | coagulating factor II receptor | 2297-2697 |
| A1e | HG886, L07594 | transforming growth factor beta receptor III 300 kDa | 3358-3592 |
| E3i | HG216, M84747 | interleukin 9 receptor | 289-528 |
| E3j | HG4080, U00672 | interleukin 10 receptor | 2448-2803 |
| E1d | HG423, M14764 | nerve growth factor receptor | 2762-3242 |
| E5d | HG1023 | Vitronectin receptor alpha subunit | 2442-2473 |
| D1b | HG125 | GATA-binding protein 2 | 1126-1363 |
| D1c | HG1377 | CCAAT-box DNA-binding protein Hap2 homolog | 958-1272 |
| C1k | HG1458 | retinoic acid receptor epsilon | 1315-1633 |
| A1f | HG1470, X13293 | B-myb | 1873-2272 |
| B1g | HG1551 | tyrosine kinase receptor tie | 3114-3536 |
| C1l | HG1601 | tyrosine kinase receptor FL T4 class III | 4236-4402 |
| D1d | HG1603 | helix-loop-helix protein 1R21 | 858-560 |
| F1j | HG1650 | thrombomodulin | 1262-1605 |
| D1e | HG1697 | basic transcription element-binding protein 2 | 572-976 |
| D1f | HG1963 | basic transcription factor 62 kDa subunit | 1449-1831 |

TABLE I (CONT)

| Array Coordinate | GeneBank # | Gene Name | Position |
|------------------|----------------|---|-----------|
| D1g | HG1972 | helix-loop-helix protein Id-2 | 111-382 |
| E4d | HG2094 | angiotensin II type 1a receptor alt splice 1 | 1855-2030 |
| B1h | HG209 | tyrosine kinase receptor HEK | 2826-3144 |
| D1h | HG2158 | DNA-binding protein SMBP2 | 1587-1911 |
| D1i | HG244 | global transcription activator | 1621-1886 |
| F1k | HG2480 | FMPLP-related receptor I | 349-657 |
| B1i | HG2490 | transmembrane receptor ror1 | 3044-3302 |
| B1j | HG2722 | tyrosine kinase KDR receptor | 2686-3053 |
| D1j | HG277 | DNA-binding protein ICS | 1253-1475 |
| A1g | HG2811 | thyroid hormone triiodothyronine receptor c-erbA ear-1 | 1676-2100 |
| D1k | HG2869 | CACCC-box DNA-binding protein | 1686-2063 |
| B1k | HG2892, X75208 | tyrosine kinase receptor | 2551-2820 |
| D1l | HG3183 | DNA-binding protein TAX | 359-765 |
| B1l | HG3314 | tyrosine kinase receptor TKT | 2621-2989 |
| B1m | L25124 | prostaglandin E2 receptor | 1818-2029 |
| E1e | HG1187 | epidermal growth factor receptor | 3410-3757 |
| E1f | HG1662 | platelet-activating factor receptor | 1103-1398 |
| B1n | HG1830 | tyrosine phosphatase receptor eph alt splice 1 | 2607-3053 |
| D1m | HG3428 | DNA-binding protein/plasminogen activator inhibitor-1 regulator | 1304-1736 |
| E3k | HG3446, A09781 | interferon gamma receptor | 66-317 |
| D1n | HG3463 | DNA-binding protein CN sterol regulating | 96-341 |
| A1h | HG3509 | v-erbA related ear-2 protein | 882-1057 |
| A1i | HG3510 | v-erbA related ear-3 protein | 1449-1700 |
| D2a | HG3548 | CCAAT displacement protein cut homolog alt splice 1 | 2000-2400 |
| D2b | HG3748 | basic transcription factor 44 kDa subunit | 606-843 |
| D2c | HG3957 | DNA-binding protein APRF | 1545-1575 |
| D2d | HG4002 | estrogen receptor hSNF2b | 2415-2682 |
| B2a | HG4196 | urokinase-type plasminogen activator receptor | 749-1043 |
| A1j | HG4269 | Ets-like gene | 710-1064 |
| B2b | HG4279 | tyrosine kinase TRK-B receptor | 1006-1384 |
| D2e | HG4574 | DNA-binding protein NFX1 cysteine-rich specific | 2003-2311 |
| A5b | HG4579 | DP2 dimerization partner of E2F | 1603-1838 |
| F1i | HG563 | glia maturation factor beta | 203-434 |
| D2i | HG753 | DNA-binding protein TAXREB67 | 1059-1495 |
| D2g | HG859, L05515 | cAMP-responsive element-binding protein | 807-1120 |
| A1k | HG898 | tyrosine kinase EGF receptor Her4 | 3570-3965 |

TABLE I (CONT)

| Array Co rdinate | GeneBank # | Gene Name | Position |
|------------------|--------------|---|-----------|
| B2c | HG918 | tyrosine phosphatase receptor gamma polypeptide | 3623-3938 |
| D2h | HG970 | DNA-binding protein PO-GA | 3196-3413 |
| D2i | HG99, M64673 | CCAAT enhancer-binding protein beta | 294-572 |
| A1i | J04111 | c-jun proto-oncogene (jun) clone HCJ-1 | 2207-2583 |
| E3i | M27492 | interleukin 1 receptor | 3847-4288 |
| C1m | M33294 | tumor necrosis factor receptor | 1570-1817 |
| F1m | M37435 | macrophage-specific colony-stimulating factor (CSF-1) | 2277-2413 |
| A1m | Y00285 | insulin-like growth factor II receptor | 1394-1831 |
| A1n | HG404 | tyrosine kinase receptor HER2 | 2556-2722 |
| B2d | D10923 | HM74 | 1357-1826 |
| B2e | D10924 | HM89 | 351-808 |
| B2f | D10925 | HM145 | 1353-1832 |
| F1n | D14012 | hepatocyte growth factor activator precursor | 1487-1845 |
| F2a | D16431 | hepatoma-derived growth factor | 359-625 |
| F2b | D30751 | bone morphogenetic protein 4 | 943-1321 |
| B2g | J03358 | FER tyrosine kinase | 2384-2688 |
| F2c | J04130 | activation (Act-2) | 236-592 |
| F2d | J05081 | endothelin ET3 | 1428-1685 |
| F2e | K03515 | neuroleukin | 1368-1656 |
| A2a | L06139 | TEK tyrosine kinase receptor | 3243-3586 |
| E1g | L06622 | endothelin receptor EDNRA | 870-1080 |
| E1h | L06623 | endothelin receptor EDNRB | 497-814 |
| F6g | L06801 | interleukin IL-13 | 285-743 |
| C1n | L07414 | CD40 ligand | 863-1277 |
| C2a | L08096 | CD27 ligand | 233-627 |
| E3m | L08187 | cytokine receptor (EB13) | 627-1019 |
| F2f | L12260 | glial growth factor 2 (recombinant) | 1069-1452 |
| F2g | L12261 | glial growth factor (recombinant) | 762-1041 |
| F6h | L15344 | interleukin IL-14 | 1181-1562 |
| F2h | L36052 | thrombopoietin (MGDF/Mpl ligand) | 230-613 |
| E1i | M10051 | insulin receptor | 3274-3758 |
| F2i | M17778 | uromodulin | 1463-1913 |
| F2j | M21121 | RANTES pro-inflammatory cytokine | 180-545 |
| E1j | M21574 | PDGF-alpha receptor | 5118-5583 |
| E1k | M21616 | PDGF-beta receptor | 842-1133 |
| F2k | M22488 | bone morphogenetic protein 1 | 702-1098 |

TABLE I (CONT)

| Array C ordinate | GeneBank # | Gene Name | Position |
|------------------|------------|---|-----------|
| F2i | M22489 | bone morphogenetic protein 2a | 567-997 |
| F2m | M22491 | bone morphogenetic protein 3 | 1458-1731 |
| F2n | M23452 | macrophage inflammatory protein GOS19-1 | 243-704 |
| F3a | M24545 | monocyte chemotactic and activating factor MCAF | 36-384 |
| F3b | M25667 | neuronal growth protein GAP-43 | 747-1154 |
| F3c | M27288 | oncostatin M | 833-1113 |
| F3d | M30704 | amphiregulin AR | 511-837 |
| F3e | M31145 | insuline-like growth factor binding protein 1 | 476-861 |
| E1i | M31165 | TNF-inducible hyaluronate-binding protein TSG-6 | 320-584 |
| F3f | M32977 | heparin-binding vascular endothelial growth factor VEGF | 198-622 |
| A2b | M35410 | insuline-like growth factor binding protein 2 | 680-1071 |
| F7a | M36717 | ribonuclease/angiogenin inhibitor RAI | 713-1028 |
| F3g | M37722 | bFGF receptor | 1746-1967 |
| B2h | M57230 | glycoprotein gp130 | 1757-2152 |
| F3h | M57399 | nerve growth factor HBNF-1 | 602-847 |
| F3i | M57502 | secreted protein I-309 | 205-397 |
| F6i | M57765 | interleukin IL-11 | 132-460 |
| E1m | M59818 | granulocyte colony-stimulating factor receptor G-CSFR1 | 1453-1891 |
| F3j | M59964 | stem cell factor | 898-1283 |
| F3k | M60278 | heparin-binding EGF-like growth factor | 1905-2146 |
| F3l | M60718 | HGF (hepatocyte growth factor) | 1549-1970 |
| F3m | M60828 | keratinocyte growth factor | 419-766 |
| F3n | M61176 | brain-derived neurotrophic factor BDNF | 982-1265 |
| F4a | M62302 | growth/differentiation factor GDF-1 | 615-957 |
| E1n | M62505 | C5a anaphylatoxin receptor | 725-1098 |
| E5e | M63928 | T cell activation antigen CD27 | 513-977 |
| F4b | M65199 | endothelin ET2 | 338-570 |
| F6j | M65290 | interleukin IL-12 (NKSF p40) | 622-848 |
| F6k | M65291 | interleukin IL-12 (NKSF p35) | 600-990 |
| C2b | M67454 | Fas antigen | 2063-2288 |
| E2a | M68932 | interleukin 8 receptor alpha (IL8RA) | 1179-1370 |
| E2b | M73482 | NMB-R (neuromedin B receptor) | 282-544 |
| F4c | M74178 | hepatocyte growth factor-like protein | 1643-2015 |
| A5c | M76125 | AXL tyrosine kinase receptor | 2054-2328 |
| E5f | M83554 | lymphocyte activation antigen CD30 | 3152-3421 |
| F4d | M92381 | thymosin beta-10 | 40-342 |

TABLE I (CONT)

| Array C ordinate | GeneBank # | Gene Name | Position |
|------------------|------------|---|-----------|
| F4e | M92934 | connective tissue growth factor | 1459-1748 |
| C2c | M93426 | tyrosine phosphatase receptor zeta-polypeptide | 5090-1748 |
| F4f | M96956 | TGDF3 | 1294-1712 |
| E2c | S59184 | RYK-related to receptor tyrosine kinase isolog | 1760-1968 |
| A2c | U01134 | VEGF receptor | 1288-1604 |
| E2d | U01839 | Duffy blood group antigen (Fya-b+) | 127-150 |
| A5d | U02687 | growth factor receptor tyrosine kinase STK-1 | 2491-2965 |
| E3n | U03187 | interleukin 12 receptor component | 1053-1381 |
| | | monocyte chemoattractant protein 1 receptor (MCP-1RA) alternatively spliced | 1514-1799 |
| E2e | U03882 | monocyte chemoattractant protein 1 receptor (MCP-1RB) alternatively spliced | 1362-1713 |
| E2f | U03905 | FLT3/FLK2 ligand | 29-362 |
| C2d | U04806 | endothelial-monocyte activating polypeptide II | 272-304 |
| F4g | U10117 | keratinocyte growth factor receptor | 753-1189 |
| E2g | U11814 | cysteine protease CPP32 isom alpha | 2007-2434 |
| C2e | U13737 | interleukin IL-15 | 338-695 |
| F6l | U14407 | activin type I receptor | 333-740 |
| E2h | U14722 | VRP (vascular endothelial growth factor related protein) | 1165-1559 |
| F4h | U43142 | IFN-gamma-inducible chemokine IP-10 | 280-613 |
| F4i | X02530 | c-kit proto-oncogene | 37-430 |
| A1d | X06182 | MRP-14 (calcium binding protein in macrophages MIF-related) | 16-254 |
| F4j | X06233 | MRP-8 (calcium binding protein in macrophages MIF-related) | 37-351 |
| F4k | X06234 | platelet-derived growth factor A chain PDGF-A | 522-955 |
| F4l | X06374 | leukemia inhibitory factor LIF | 1810-2239 |
| F4m | X13967 | interleukin IL-9 (P40) | 156-186 |
| F6m | X17543 | granulocyte-macrophage colony-stimulating factor receptor GM-CSFRa | 868-1173 |
| E2i | X17648 | fibroblast growth factor FGF-1 | 1131-1502 |
| F4n | X51943 | nerve growth factor NGF-2 (same as NT-3) | 112-416 |
| F5a | X53655 | macrophage inflammatory protein-2alpha (MIP2alpha) | 157-501 |
| F5b | X53799 | PIGF (placenta growth factor) | 1098-1371 |
| F5c | X54936 | interleukin 1 receptor type II | 842-1244 |
| E4a | X59770 | Cd44 | 198-605 |
| E2j | X60592 | beta-thromboglobulin-like protein | 230-533 |
| E2k | X72304 | neutrophil-activating peptide ENA-78 | 65-329 |
| F5d | X78686 | OX40 ligand/gp34 | 329-657 |
| F5e | X79929 | | |

TABLE I (CONT)

| Array Coordinate | GeneBank # | Gene Name | Position |
|------------------|------------|---|-----------|
| F5i | Y00787 | monocyte-derived neutrophil chemotactic factor MDNCF | 99-287 |
| B2i | D10495 | protein kinase C delta-type | 1467-1817 |
| D2j | D13316 | transcription factor E4TF1-47 | 965-1175 |
| D2k | D13318 | transcription factor E4TF1-60 | 1069-1512 |
| C5i | D13804 | recA-like protein HsRad51 | 867-1159 |
| E5g | D13866 | alpha-catenin | 2235-2577 |
| A5e | D13889 | Id-1H | 83-433 |
| D2l | D15050 | transcription factor AREB6 | 2417-2680 |
| C2f | D15057 | DAD-1 | 124-334 |
| A2d | D17517 | sky Sky | 2132-2597 |
| B2j | D21878 | BST-1 | 706-980 |
| D2m | D26120 | ZFM1 protein | 2367-2704 |
| D2n | D26121 | ZFM1 protein alternatively spliced product | 440-908 |
| D3a | D26155 | transcriptional activator hSNF2a | 3917-4258 |
| B2k | D26309 | LIMK (LIM kinase) | 2810-3157 |
| D3b | D28118 | DB1 | 1166-1481 |
| D3c | D28468 | DNA-binding protein TAXREB302 | 386-811 |
| E5h | J03132 | intercellular adhesion molecule-1 (ICAM-1) | 1220-1599 |
| A2e | J03241 | transforming growth factor-beta 3 (TGF-beta3) | 1416-1833 |
| F7b | J03634 | erythroid differentiation protein (EDF) | 983-1372 |
| E5i | J04536 | sialophorin (CD43) | 178-392 |
| C5j | L04791 | excision repair protein ERCC6 | 1772-2194 |
| B2l | L05624 | MAP kinase kinase | 842-1217 |
| C5k | L07540 | replication factor C 36-kDa subunit | 708-1051 |
| C5l | L07541 | replication factor C 38-kDa subunit | 438-762 |
| D3d | L08424 | achaete scute homologous protein (ASH1) | 1113-1455 |
| A2f | L11353 | moesin-ezrin-radixin-like protein | 355-674 |
| D3e | L11672 | Kruppel related zinc finger protein (HTF10) | 107-555 |
| B2m | L13616 | focal adhesion kinase (FAK) | 2179-2631 |
| B2n | L13738 | activated p21cdc42Hs kinase (ack) | 758-1184 |
| A5f | L13740 | TR3 orphan receptor | 818-1077 |
| D3f | L14611 | transcription factor RZR-alpha | 620-982 |
| A2g | L14837 | tight junction (zonula occludens) protein ZO-1 (tumor suppressor) | 6327-6660 |
| C2g | L16785 | c-myc transcription factor (puf) | 69-351 |
| B3a | L19067 | NF-kappa-B transcription factor p65 subunit | 1897-2137 |
| B7h | L19185 | natural killer cell enhancing factor (NKEFB) | 348-736 |

TABLE I (CONT)

| Array Coordinate | GeneBank # | Gene Name | Position |
|------------------|------------|--|-----------|
| D3g | L19606 | paired box homeotic protein (PAX8) | 113-338 |
| C5m | L20046 | ERCC5 excision repair protein | 1374-1638 |
| B3b | L20320 | protein serine/threonine kinase sk1 | 89-305 |
| B3c | L20321 | protein serine/threonine kinase sk2 | 2534-2802 |
| B3d | L20422 | 14-3-3n protein | 163-671 |
| D3h | L20433 | octamer binding transcription factor 1 (OTF1) | 3275-3583 |
| E5j | L20815 | S protein | 1677-2107 |
| B1a | L20977 | plasma membrane calcium ATPase isoform 2 (ATP2B2) | 3861-4236 |
| B3e | L22075 | guanine nucleotide regulatory protein (G13) | 1073-1376 |
| C2h | L22474 | Bax beta | 227-278 |
| C5n | L24564 | Rad | 489-780 |
| B3f | L24959 | calcium/calmodulin dependent protein kinase | 969-1220 |
| B3g | L25259 | CTLA4 counter-receptor (B7-2) | 496-722 |
| C2i | L29511 | GRB2 isoform | 355-573 |
| D3i | L31881 | nuclear factor I-X | 415-729 |
| B3h | L32976 | protein kinase (MLK-3) | 970-1283 |
| A5g | L33264 | CDC2-related protein kinase (PISSLRE) | 454-755 |
| D3j | L34587 | RNA polymerase II elongation factor SIII p15 subunit | 115-354 |
| B3i | L35233 | autocrine motility factor receptor (AMFR) | 1221-1514 |
| A2h | M13150 | mas proto-oncogene | 262-726 |
| D3k | M14631 | guanine nucleotide-binding protein G-s alpha subunit partial cds | 824-1120 |
| B1b | M15800 | MAL protein | 461-695 |
| D3l | M16937 | homeobox c1 protein | 367-667 |
| E5k | M21097 | differentiation antigen (CD19) | 740-1071 |
| B3j | M22199 | protein kinase C alpha-polypeptide (PKCA) | 767-1106 |
| E5l | M23197 | differentiation antigen (CD33) | 885-1141 |
| A5h | M26708 | prothymosin alpha (ProT-alpha) | 538-864 |
| B3k | M28210 | GTP-binding protein (RAB3A) | 288-591 |
| B3l | M28211 | GTP-binding protein (RAB4) | 255-495 |
| B3m | M28212 | GTP-binding protein (RAB6) | 59-310 |
| B3n | M28213 | GTP-binding protein (RAB2) | 56-269 |
| B4a | M28214 | GTP-binding protein (RAB3B) | 322-621 |
| B4b | M28215 | GTP-binding protein (RAB5) | 447-672 |
| A5i | M28882 | MUC18 glycoprotein | 1756-2180 |
| D3m | M29038 | stem cell protein (SCL) | 2804-3086 |
| A5j | M29142 | myeloblastin | 312-693 |

TABLE I (CONT)

| Array Coordinate | GeneBank # | Gene Name | Position |
|------------------|------------|---|-----------|
| E5m | M30257 | vascular cell adhesion molecule 1 | 1056-1450 |
| E5n | M30640 | endothelial leucocyte adhesion molecule 1 (ELAM1) | 2098-2549 |
| C6a | M30938 | Ku (p70/p80) subunit | 2340-2764 |
| A2i | M31213 | papillary thyroid carcinoma-encoded protein | 2285-2631 |
| D3n | M31523 | transcription factor (E2A) | 2277-2685 |
| B4c | M31630 | cyclic AMP response element-binding protein (HB16) 3' end | 316-636 |
| C6b | M31899 | DNA repair helicase (ERCC3) | 2109-2466 |
| C6c | M32865 | Ku protein subunit | 1729-1974 |
| E6a | M33374 | cell adhesion protein (SQM1) | 53-354 |
| E6b | M34064 | N-cadherin | 942-1299 |
| B4d | M34356 | active transcription factor CREB | 433-780 |
| D4a | M34960 | transcription factor IID | 561-843 |
| C6d | M36089 | DNA-repair protein (XRCC1) | 1226-1539 |
| B4e | M36429 | transducin beta-2 subunit | 443-789 |
| B4f | M36430 | transducin beta-1 subunit 3' end | 58-338 |
| D4b | M36542 | lymphoid-specific transcription factor | 647-942 |
| D4c | M36711 | sequence-specific DNA-binding protein (AP-2) | 950-1211 |
| A2j | M54915 | h-pim-1 protein (h-pim-1) | 893-1187 |
| E6c | M54992 | B cell differentiation antigen | 963-1224 |
| E6d | M59040 | cell adhesion molecule (CD44) | 1158-1408 |
| A2k | M60915 | neurofibromatosis protein type I (NF1) | 740-1027 |
| D4d | M62397 | colorectal mutant cancer protein | 3626-3902 |
| D4e | M62810 | mitochondrial transcription factor 1 | 640-668 |
| D4f | M62829 | transcription factor ETR103 | 989-1276 |
| D4g | M62831 | transcription factor ETR101 | 1018-1410 |
| C6e | M63488 | replication protein A 70kDa subunit | 1498-1838 |
| A5k | M63618 | bulbous pemphigoid antigen | 5680-6055 |
| D4h | M63896 | transcriptional enhancer factor (TEF1) DNA | 2935-3238 |
| E6e | M74387 | cell adhesion molecule L1 (L1CAM) | 3197-3483 |
| C6f | M74524 | HH-R6A (yeast RAD 6 homologue) | 175-433 |
| E6f | M74777 | dipeptidyl peptidase IV (CD26) | 1205-1507 |
| C2j | M74816 | sulfated glycoprotein-2 3' end | 709-990 |
| D4i | M75952 | homeobox protein (HOX-11) | 1209-1552 |
| D4j | M76541 | DNA-binding protein (NF-E1) | 706-1053 |
| D4k | M76766 | transcription factor (TFIIB) | 407-769 |
| D4l | M80627 | HEB helix-loop-helix protein (HEB) | 3676-3984 |

TABLE I (CONT)

| Array Coordinate | GeneBank # | Gene Name | Position |
|------------------|------------|--|-----------|
| D4m | M81601 | transcription elongation factor (SII) | 227-593 |
| A2l | M81750 | myeloid cell nuclear differentiation antigen | 549-873 |
| A5l | M81757 | S19 ribosomal protein | 113-408 |
| D4n | M81840 | NRL gene product | 946-1158 |
| D5a | M83234 | nuclease-sensitive element DNA-binding protein | 790-1099 |
| C2k | M84820 | retinoid X receptor beta (RXR-beta) | 643-1135 |
| C6g | M87338 | replication factor C 40-kDa subunit (A1) | 882-1286 |
| C6h | M87339 | replication factor C 37-kDa subunit | 98-355 |
| D5b | M87503 | IFN-responsive transcription factor subunit | 1057-1520 |
| D5c | M92299 | homeobox 21 protein (HOX2A) | 1718-1945 |
| D5d | M92843 | zinc finger transcriptional regulator | 892-1271 |
| D5e | M93255 | FLI-1 | 728-1118 |
| E4e | M95489 | follicle stimulating hormone receptor | 1507-1752 |
| D5f | M96824 | nucleobindin precursor | 701-1068 |
| D5g | M96944 | B-cell specific transcription factor (BSAP) | 2446-2771 |
| D5h | M97287 | MAR/SAR DNA binding protein (SATB1) | 1921-2226 |
| D5i | M97676 | (region 7) homeobox protein (HOX7) | 1091-1450 |
| E4h | S64045 | 5HT1a=5-hydroxytryptamine receptor (transmembrane regions 5 and 6) | 128-413 |
| A5m | U01160 | transmembrane 4 superfamily protein (SAS) | 98-409 |
| B4g | U02081 | guanine nucleotide regulatory protein (NET1) | 1079-1323 |
| B4h | U02082 | guanine nucleotide regulatory protein (tim1) | 1852-2185 |
| D5j | U02326 | clone ndf43 neu differentiation factor | 1430-1701 |
| D5k | U02368 | PAX3/forkhead transcription factor fusion | 2231-2569 |
| D5l | U02619 | TFIIIC Box B-binding subunit | 5023-5369 |
| D5m | U02683 | alpha palindromic binding protein | 1630-2062 |
| A2m | U03056 | tumor suppressor (LUCA-1) | 2039-2444 |
| D5n | U03494 | transcription factor LSF | 1358-1681 |
| B4i | U03688 | dioxin-inducible cytochrome P450 (CYP1B1) | 1212-1556 |
| D6a | U04847 | Ini1 | 125-538 |
| D6b | U05040 | FUSE binding protein | 1002-1339 |
| A5n | U05340 | p55CDC | 1236-1522 |
| B4j | U05875 | clone pSK1 interferon gamma receptor accessory factor-1 (AF-1) | 1702-2039 |
| B1c | U07139 | voltage-gated calcium channel beta subunit | 2008-2383 |
| B4k | U07236 | mutant lymphocyte-specific protein tyrosine kinase (LCK) | 930-1207 |
| A6a | U07616 | amphiphysin | 1740-2143 |
| B4l | U07707 | epidermal growth factor receptor substrate (eps15) | 1828-2140 |

TABLE I (CONT)

| Array Coordinate | GeneBank # | Gene Name | Position |
|------------------|------------|--|-----------|
| E6g | U07819 | contactin 1 precursor (CNTN1) | 2735-3130 |
| D6c | U08015 | NF-ATc | 2039-2374 |
| D6d | U08191 | R kappa B | 4657-4920 |
| D6e | U08853 | transcription factor LCR-F1 | 1575-1928 |
| B4m | U09564 | serine kinase | 487-833 |
| D6f | U09579 | melanoma differentiation associated (mda-6) | 1745-2063 |
| B4n | U09607 | JAK family protein tyrosine kinase JAK3 | 3556-3892 |
| D6g | U10323 | nuclear factor NF-45 | 967-1380 |
| D6h | U10324 | nuclear factor NF-90 | 2901-3146 |
| D6i | U10421 | HOX A1 homeodomain protein (HOXA1) | 132-492 |
| D6j | U12535 | epidermal growth factor receptor kinase substrate (Eps8) | 2293-2645 |
| C2l | U13021 | positive regulator of programmed cell death ICH-1L (Ich-1) | 851-1218 |
| D6k | U13897 | homolog of Drosophila discs large protein isoform 1 (hdlg-1) | 2248-2624 |
| D6l | U14575 | (ard-1) | 665-942 |
| D6m | U14755 | LIM domain transcription factor LIM-1 (hLIM-1) | 479-759 |
| D6n | U15979 | (dlk) | 1090-1403 |
| B5a | U16031 | transcription factor IL-4 stat | 1816-2118 |
| C6i | X06745 | DNA polymerase alpha-subunit | 3721-4093 |
| A2n | X07024 | X chromosome CCG1 protein inv in cell proliferation | 4002-4343 |
| A3a | X15218 | ski oncogene | 2354-2662 |
| A3b | X15219 | sno oncogene snoN protein ski-related | 2224-2652 |
| E6h | X16841 | N-CAM (a nontransmembrane isoform) from skeletal muscle | 2338-2646 |
| A3c | X51630 | Wilms tumor WT1 zinc finger protein Krueppel-like | 1866-2254 |
| D7a | X55122 | GATA-3 transcription factor | 1097-1383 |
| A6b | X55504 | P120 antigen | 1970-2245 |
| D7b | X59738 | ZFX put transcription activator isoform 1 | 749-1113 |
| D7c | X67951 | proliferation-associated gene (pag) | 543-856 |
| B5b | X70326 | MacMarcks | 638-1008 |
| B5c | X74979 | TRK E | 2138-2411 |
| E6i | Z26317 | desmoglein 2 | 2819-3135 |
| F7c | A00914 | angiotensin-converting enzyme (ACE) | 2123-2483 |
| F7d | A06925 | relaxin H2 | 123-427 |
| F7e | D10232 | renin-binding protein | 289-589 |
| E4i | D28538 | glutamate receptor type 1 subtype 5a | 3745-4027 |
| F7i | J04040 | glucagon | 201-540 |
| E4j | L19058 | glutamate receptor 5 | 2514-2779 |

TABLE I (CONT)

| Array Coordinate | GeneBank # | Gene Name | Position |
|------------------|------------|---|-----------|
| F7g | M13981 | inhibin A-subunit | 828-1183 |
| F7h | M14200 | diazepam binding inhibitor | 67-257 |
| E4k | M15169 | Beta-2-adrenergic receptor | 2412-2783 |
| E4l | M29066 | dopamine d2 receptor | 1226-1521 |
| F7i | M31159 | growth hormone-dependent insulin-like growth factor-binding protein | 451-744 |
| F7j | M68867 | retinoic acid-binding protein II | 489-863 |
| E4m | M76446 | alpha A1 adrenergic receptor | 1599-1942 |
| E4n | M86841 | serotonin receptor type 2 | 938-1239 |
| F7k | U06863 | folistatin-related protein precursor | 1093-1425 |
| F7l | X58022 | corticotropin-releasing factor-binding protein | 853-1140 |
| A6c | HT0121 | cyclin-dependent kinase 2 | 1774-2180 |
| A6d | HT0191 | cell division cycle protein 25A tyrosine phosphatase | 1632-1978 |
| A6e | HT0285 | cyclin D3 | 537-894 |
| C6j | HT330 | single-stranded DNA-binding protein pur-alpha | 563-855 |
| A6f | HT0609 | cyclin A | 876-1218 |
| C6k | HT767 | DNA topoisomerase I | 2388-2796 |
| C6l | HT784 | DNA topoisomerase II alpha | 2459-2863 |
| C6m | HT1104 | 6-O-methylguanine-DNA methyltransferase | 241-546 |
| C6n | HT1175 | DNA excision repair protein ERCC2 5' end | 1520-1821 |
| A3d | HT1426 | prohibitin | 172-455 |
| A3e | HT1436 | proto-oncogene raf | 1704-1989 |
| C2m | HT1483 | glutathione reductase | 719-1057 |
| A3f | HT1489 | proto-oncogene c-abl tyrosine protein kinase alt transcript 1 | 3240-3612 |
| A6g | HT1547 | cyclin D1 | 3427-3784 |
| C2n | HT1790 | glutathione S-transferase 12 | 72-420 |
| C7a | HT1848 | DNA excision repair protein ERCC1 alt transcript 1 | 625-938 |
| C3a | HT2041 | glutathione S-transferase M1 | 504-906 |
| C3b | HT2042 | glutathione S-transferase pi | 203-511 |
| C3c | HT2168 | glutathione S-transferase A1 | 257-583 |
| A6h | HT2181 | cyclin D2 | 3932-4284 |
| A3g | HT2291 | proto-oncogene c-src1 tyrosine kinase domain | 893-1189 |
| A3h | HT2788 | proto-oncogene rel | 1357-1605 |
| A3i | HT2856 | proto-oncogene rhoA multidrug resistance protein | 290-572 |
| C3d | HT2859 | glutathione peroxidase | 454-745 |
| A3j | HT3039 | proto-oncogene shb src-2 homolog | 1365-1657 |
| C3e | HT3190 | apoptosis regulator bcl-x | 412-676 |

TABLE I (CONT)

| Array Co rdinate | GeneBank # | Gene Name | Position |
|------------------|----------------|---|-----------|
| C7b | HT3218 | superoxide dismutase 1 cytosolic | 198-486 |
| C7c | HT3337 | DNA mismatch repair protein hmlh1 | 1765-2020 |
| A6i | HT3410 | cell division cycle protein 25 nucleotide exchange factor | 3372-3651 |
| A3k | HT3563 | tumor suppressor DCC colorectal | 3749-4042 |
| C3f | HT3614 | cytochrome P450 reductase | 789-1082 |
| | | xeroderma pigmentosum group C repair complementing protein | |
| C7d | HT4209 | p58/HHR23B | 582-885 |
| C7e | HT4247 | xeroderma pigmentosum group C repair complementing protein HHR23A | 355-632 |
| A6j | HT4540 | cyclin H | 717-1026 |
| C3g | HT4547 | glutathione S-transferase T1 | 617-914 |
| C3h | HT5168 | ionizing radiation resistance-conferring protein | 856-1114 |
| E6j | J02703 | endothelial membrane glycoprotein IIIA (GPIIIA) | 2038-2373 |
| E6k | J04145 | neutrophil adherence receptor alpha-M subunit | 2888-3183 |
| E6l | J05633 | integrin beta-5 subunit | 2279-2528 |
| E6m | L12002 | integrin alpha 4 subunit | 2709-3063 |
| E6n | M15395 | leukocyte adhesion protein (LFA-1/MAC-1/P15095 family) beta subunit | 2367-2664 |
| E7a | M34480 | platelet glycoprotein IIb (GPIIb) | 268-639 |
| E7b | M35198, J05522 | integrin B-6 | 1619-1901 |
| E7c | M59911 | integrin alpha-3 chain | 2562-2944 |
| E7d | M81695, Y00093 | leukocyte adhesion glycoprotein P15095 | 88-271 |
| E7e | X06256 | fibronectin receptor alpha subunit | 2094-2367 |
| E7f | X07979 | fibronectin receptor beta subunit | 2116-2482 |
| E7g | X53586 | integrin alpha 6 | 3642-3988 |
| E7h | X53587 | integrin beta 4 | 5357-5697 |
| E7i | X68742 | integrin alpha subunit | 2690-2976 |
| E7j | X74295 | alpha 7B integrin | 255-591 |
| E7k | Y00796 | leukocyte-associated molecule-1 alpha subunit (LFA-1 alpha subunit) | 4526-4856 |
| C3i | D38122 | Fas ligand | 516-840 |
| B7i | D49547 | heat-shock protein 40 | 1400-1782 |
| D7d | J03133 | transcription factor SP1 3' end | 1876-2272 |
| B5d | L07032 | protein kinase C theta (PKC) | 2306-2601 |
| B5e | L26318 | protein kinase (JNK1) | 952-1263 |
| A6k | L27211 | CDK4-inhibitor (p16-INK4) | 482-836 |
| B5f | L35253 | p38 mitogen activated protein (MAP) kinase | 925-1204 |
| B5g | L36719 | MAP kinase kinase 3 (MKK3) | 790-1169 |
| B5h | L36870 | MAP kinase kinase 4 (MKK4) | 2788-3103 |

TABLE I (CONT)

| Array Coordinate | GeneBank # | Gene Name | Position |
|------------------|------------|---|-------------|
| C3j | M13228 | N-myc oncogene protein | 761-1188 |
| A3i | M15400 | retinoblastoma susceptibility | 2839-3101 |
| A3m | M15990 | c-yes-1 | 1325-1676 |
| B5i | M16038 | "lyn, tyrosine kinase" | 1393-1666 |
| A3n | M19720 | L-myc protein | 5847-6118 |
| A4a | M19722 | lgr proto-oncogene encoded p55-c-fgr protein | 521-856 |
| A6i | M25753 | cyclin B | 979-1311 |
| B5j | M27545 | protein kinase C (PKC) type beta I | 1561-1821 |
| B5k | M31158 | cAMP-dependent protein kinase subunit RII-beta | 1305-1506 |
| B7j | M34664 | chaperonin (HSP60) | 533-839 |
| B5l | M35203 | protein-tyrosine kinase (JAK1) | 2768-3054 |
| C7i | M60974 | growth arrest and DNA-damage-inducible protein (gadd45) | 526-886 |
| B5m | M65066 | cAMP-dependent protein kinase regulatory subunit RI-beta 3' end | 444-662 |
| A6m | M73812 | cyclin E | 1295-1658 |
| A4b | M74088 | APC | 7992-8326 |
| D7e | M83221 | I-Rel | 853-1129 |
| B5n | M84489 | extracellular signal-regulated kinase 2 | 1241-1522 |
| D7i | M97190 | Sp2 protein | 396-682 |
| D7g | M97191 | Sp3 protein | 1588-1987 |
| C7g | S40706 | GADD153=growth arrest and DNA-damage-inducible | 480-789 |
| C3k | U25994 | cell death protein (RIP) | 848-1123 |
| B6a | U30473 | putative src-like adapter protein (SLAP) | 524-901 |
| C7h | U35835 | DNA-PK | 2250-2680 |
| A6n | U40343 | CDK inhibitor p19INK4d | 750-952 |
| E7i | U43522 | cell adhesion kinase beta (CAKbeta) | 3658-3952 |
| A4c | U43746 | breast cancer susceptibility (BRCA2) | 10056-10346 |
| A7a | U47413 | cyclin G1 | 755-1035 |
| A7b | U47414 | cyclin G2 | 989-1254 |
| A7c | U66838 | cyclin A1 | 1205-1456 |
| A4d | X02751 | N-ras | 708-1064 |
| B7k | X07270 | heat shock protein hsp86 | 380-577 |
| B6b | X07767 | cAMP-dependent protein kinase catalytic subunit type alpha (EC 27137) | 460-740 |
| A4e | X16706 | fra-2 | 376-663 |
| A4f | X16707 | fra-1 | 617-897 |
| A4g | X51521 | ezrin | 1611-1883 |
| B7l | X54079 | heat shock protein HSP27 | 423-663 |

TABLE I (CONT)

| Array Co rdinate | GeneBank # | Gene Name | Position |
|------------------|------------|--|-----------|
| B6c | X54637 | tyk2 non-receptor protein tyrosine kinase | 3787-4110 |
| A4h | X56681 | junD | 508-780 |
| A4i | X59932 | c-src-kinase | 488-876 |
| B6d | X60188 | ERK1 protein serine/threonine kinase | 754-1094 |
| B6e | X80692 | ERK3 | 806-1267 |
| C3i | X86779 | FAST kinase | 865-1239 |
| E7m | X87838 | beta-catenin | 2061-2463 |
| C3m | X89986 | NBK apoptotic inducer protein | 935-1200 |
| A7d | X92669 | p35 cyclin-like CAK1-associated protein | 39-237 |
| B6f | Z29090 | phosphatidylinositol 3-kinase | 3021-3283 |
| C3n | L11015 | lymphotoxin-beta | 69-429 |
| B6g | L31951 | protein kinase (JNK2) | 638-1000 |
| B6h | L34583 | tyrosine phosphatase (clone HFAP10) | 1372-1701 |
| C4a | L41690 | TNF receptor-1 associated protein (TRADD) | 1009-1313 |
| C4b | M14745 | bcl-2 | 5087-5382 |
| C4c | U15172 | NIP1 (NIP1) | 412-719 |
| C4d | U15174 | NIP3 (NIP3) | 272-637 |
| C4e | U20537 | cysteine protease MCH2 isom beta (MCH2) | 387-697 |
| C4f | U23765 | BAK protein | 1371-1661 |
| C4g | U28014 | cysteine protease (ICEREL-II) | 763-1107 |
| C4h | U29680 | A1 protein | 64-293 |
| B6i | U34819 | JNK3 alpha2 protein kinase (JNK3A2) | 1018-1413 |
| C4i | U45878 | inhibitor of apoptosis protein 1 | 1444-1848 |
| C4j | U45879 | inhibitor of apoptosis protein 2 | 2000-2363 |
| C4k | U45880 | X-linked inhibitor of apoptosis protein XIAP | 266-621 |
| C4l | U56390 | cysteine protease ICE-LAP6 | 986-1289 |
| C4m | U57059 | Apo-2 ligand | 211-616 |
| C4n | U60519 | apoptotic cysteine protease Mch4 (Mch4) | 2276-2690 |
| C5a | U60520 | apoptotic cysteine protease Mch5 isom alpha (Mch5) | 1327-1607 |
| B6j | X14454 | interferon regulatory factor 1 | 478-695 |
| C5b | X96586 | FAN protein | 2449-2726 |
| C5c | Y09392 | WSL-LR WSL-S1 and WSL-S2 proteins | 1407-1671 |
| D7h | D11117 | homeobox HOX 4A homeodomain protein | 4200-4447 |
| A7e | D38305 | Tob | 626-926 |
| B6k | D42108 | phospholipase C | 1635-2003 |
| D7i | D45132 | zinc-finger DNA-binding protein | 5113-5551 |

TABLE I (CONT)

| Array Coordinate | GeneBank # | Gene Name | Position |
|------------------|------------|---|-----------|
| E5a | D49394 | serotonin 5-HT3 receptor | 1703-2000 |
| A4j | L16464 | ETS oncogene (PEP1) | 418-711 |
| A7f | L29216 | CLK2 | 1106-1356 |
| A7g | L29220 | CLK3 | 551-1002 |
| A7h | L29222 | CLK1 | 144-459 |
| E5b | L76224 | NMDA receptor | 2097-2395 |
| B7m | M11717 | heat shock protein (HSP 70) | 1962-2225 |
| F5g | M27544 | insulin-like growth factor | 652-919 |
| B6l | M68516 | protein C inhibitor | 8035-8423 |
| F5h | M86528 | neurotrophin-4 (NT-4) | 721-1079 |
| B6m | U09578 | MAPKAP kinase (3pK) | 486-837 |
| A7i | U10564 | CDK tyrosine 15-kinase WEE1HU (WEE1HU) | 1259-1502 |
| C7i | U12134 | DNA damage repair and recombination protein RAD52 | 1528-1733 |
| B6n | U14187 | receptor tyrosine kinase ligand LERK-3 (EPLG3) | 175-566 |
| B7a | U14188 | receptor tyrosine kinase LERK-4 (EPLG4) | 169-436 |
| B7b | U18087 | 3'-cAMP phosphodiesterase HPDE4A6 | 1119-1453 |
| C5d | U21092 | CD40 receptor associated factor 1 (CRAF1) | 980-1322 |
| A7j | U22398 | CDK-inhibitor P57KIP2 (KIP2) | 1048-1316 |
| A4k | U24166 | EB1 | 488-796 |
| A4l | U26710 | CBL-B | 3054-3444 |
| D7j | U28838 | transcription factor TFIIB 90 kDa subunit (HTFIIB90) | 2336-2605 |
| D7k | M30504 | transcription initiation factor TFIID subunit TAFI31 | 260-638 |
| F6n | U32659 | IL-17 | 257-578 |
| C5e | U32944 | cytoplasmic dynein light chain 1 (hdcl1) | 48-265 |
| B7c | U33635 | colon carcinoma kinase-4 (CCK4) | 3507-3784 |
| C7j | U33841 | ataxia telangiectasia (ATM) | 8938-9135 |
| A7k | U35735 | RACH1 (RACH1) | 1072-1391 |
| C5f | U39613 | cysteine protease ICE-LAP3 | 541-844 |
| B7d | U39657 | MAP kinase kinase 6 (MKK6) | 1060-1389 |
| B7e | U40282 | integrin-linked kinase (ILK) | 1245-1530 |
| A7l | U41816 | C-1 | 143-356 |
| D7l | U43188 | Ets transcription factor (NERF-2) | 1967-2400 |
| B7f | U43408 | tyrosine kinase (Tnk1) | 1455-1849 |
| A4m | U57456 | transforming growth factor-beta signaling protein-1 (bsp-1) | 1417-1679 |
| C5g | U59747 | Bcl-w (bcl-w) | 121-403 |
| D7m | U59863 | TRAF-interacting protein I-TRAF | 674-887 |

TABLE I (CONT)

| Array Coordinate | GeneBank # | Gene Name | Position |
|------------------|----------------|---|-----------|
| E7n | U60800 | semaphorin (CD100) | 2517-2921 |
| A4n | U61262 | neogenin | 3144-3573 |
| C7k | U63139 | Rad50 (Rad50) | 5117-5435 |
| A5a | U68162 | thrombopoietin receptor (MPL) | 2184-2448 |
| C5h | U71364 | serine proteinase inhibitor (P19) | 618-986 |
| C7l | X83441 | DNA ligase IV | 2787-3074 |
| C7m | X84740 | DNA ligase III | 2460-2780 |
| C7n | X90392 | DNase X | 2038-2427 |
| B7n | HT4197 | glutaredoxin | 43-325 |
| F7m | U08098 | estrogen sulfotransferase (STE) | 533-852 |
| F7n | X54469, M28019 | beta-preprotachykinin | 321-7888 |
| B7g | L25876 | protein tyrosine phosphatase (CIP2) | 110-499 |
| A7m | M81934 | CDC25B | 2286-2602 |
| A7n | U17075 | P14-CDK inhibitor | 116-462 |
| G12 | X01677 | LIVER GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE | 663-932 |
| G13 | K00558 | TUBULIN ALPHA | |
| G14 | M11886 | HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, C-4 ALPHA CHAIN [MHC] | |
| G19 | X00351 | BETA-ACTIN | 692-1077 |
| G20 | X56932 | 23 kDa HIGHLY BASIC PROTEIN | |
| G21 | U14971 | RIBOSOMAL PROTEIN S9 | |
| G5 | M26880 | UBIQUITIN | 1922-2181 |
| G6 | M86400 | PHOSPHOLIPASE A2 | |
| G7 | V00530 | HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE | |

Mouse Array

In the mouse array according to the subject invention, all of the unique polynucleotide probe compositions will correspond to a mouse gene of interest. Mouse genes that are represented on the array are key genes, by which is meant that they have been reported to play primary roles in a variety of different biological processes. Typically the mouse genes represented on the array are genes that are under tight transcriptional control. Genes of interest that may be represented on the array include: oncogenes, cell cycle genes, apoptosis genes, growth factor genes, cytokine genes, interleukin genes, receptor genes, and genes associated with different stages of embryonic development.

10 In certain embodiments, of particular interest is an array having the following types of genes represented on its surface: oncogenes & tumor suppressors; cell cycle regulators; stress response proteins; ion channel & transport proteins; intracellular signal transduction modulators & effectors; apoptosis-related proteins; DNA synthesis, repair & recombination proteins; transcription factors & general DNA binding proteins; growth factor & chemokine receptors; interleukin & interferon receptors, hormone receptors; neurotransmitter receptors; cell-surface antigens & cell adhesion proteins; interleukins & interferons; cytoskeleton & motility proteins; and protein turnover. In a specific mouse array of interest, the spots are as listed in Table 2.

20 The mouse array of the subject invention finds use in a variety of different applications, where such applications include: profiling differential gene expression in transgenic knockout mice or other experimental mouse models; investigating processes such as embryo genesis and tumorigenesis; discovering potential therapeutic and diagnostic drug targets; and the like.

TABLE 2

| GenBank # | Gene Name | Array Coordinate | Position |
|-----------|---|------------------|-----------|
| D13473 | MmRad51; yeast DNA repair protein Rad51 and E coli RecA homologue | C6m | 855-1199 |
| D17630 | Interleukin-8 receptor | E3h | 664-1022 |
| D25281 | Catenin alpha | E5m | 1276-1594 |
| D31788 | BST-1; lymphocyte differentiation antigen CD38 | B2h | 674-1014 |
| D31942 | Oncostatin M | F3n | 1017-1360 |
| L05630 | C5A receptor | E1g | 841-1165 |
| L07264 | Heparin-binding EGF-like growth factor (Diphtheria toxin receptor) | F2d | 258-673 |
| U04807 | Fms-related tyrosine kinase 3 Flt3/Flk2 ligand | C3i | 46-418 |
| L24495 | CD27; lymphocyte-specific NGF receptor family member | C2l | 596-846 |
| M28998 | Fibroblast growth factor receptor Basic (b FGF-R) | E2c | 200-583 |
| M58288 | Granulocyte colony - stimulatings factor receptor | E1j | 251-529 |
| M62301 | Growth/ differentiation factor 1 (GDF-1) (TGF- beta family) | F2b | 2267-2566 |
| M69042 | PKC-delta; protein kinase C delta type | B6g | 1740-2011 |
| M74517 | GA binding protein beta-2 chain | D3d | 613-931 |
| M83312 | CD 40L receptor (TNF receptor family) | E1f | 417-754 |
| M83649 | FasL receptor (Fas antigen, Apo-1 antigen) | C3f | 416-736 |
| M86671 | Interleukin 12 (p40) beta chain | F4n | 652-963 |
| M95200 | Vascular endothelial growth factor (VEGF) | F4j | 688-955 |
| U03421 | Interleukin 11 (adipogenesis inhibitory factor) | F4m | 196-475 |
| U14332 | Interleukin 15 | F5a | 605-1057 |
| U15159 | LIMK; LIM serine/threonine kinase | B5l | 1376-1699 |
| U83628 | DAD-1; defender against cell death 1 | C3d | 221-509 |
| U25416 | CD 30L receptor (Lymphocyte activation antigen CD 30, Ki-1 antigen) | C2m | 135-435 |
| U44725 | Mast cell factor | F3i | 79-417 |
| U56819 | C-C chemokine receptor (Monocyte chemoattractant protein 1 receptor (MCP-1RA) | E1d | 965-1262 |
| X06381 | Leukemia inhibitory factor (LIF) (cholinergic differentiation factor) | F3d | 63-366 |
| X52264 | Intercellular adhesion molecule-1 | E7i | 1053-1385 |
| X59769 | Interleukin-1 receptor type II | E2n | 883-1134 |
| X72305 | Corticotropin releasing factor receptor | E1h | 1411-1748 |
| X72307 | Hepatocyte growth factor (hepapoitein) | F2e | 641-965 |
| Z22703 | Keratinocyte growth factor FGF-7 | F3b | 63-325 |
| Z31663 | Activin type I receptor | E1a | 847-1130 |

TABLE 2 (CONT)

| GenBank # | Gene Name | Array Coordinate | Position |
|-----------|--|------------------|-----------|
| D01034 | Transcription factor TF II D | B4j | 291-556 |
| D14340 | ZO-1; Tight junction protein; discs-large family member, partially homologous to a dlg-A tumor suppressor in <i>Drosophila</i> | A2d | 3714-4001 |
| D16306 | ERCC5 excision repair protein; DNA-repair protein complementing XP-G cells (XPG) | C6f | 1336-1639 |
| L22472 | Bax; Bcl-2 heterodimerization partner and homologue | C1g | 172-534 |
| L25606 | B7-2; T lymphocyte activation antigen CD86; CD28 antigen ligand 2, B7-2 antigen; alternative CTLA4 counter-receptor | B2g | 570-967 |
| L27105 | NF2; Merlin (moesin-ezrin-radixin-like protein); shwannomin, murine neurofibromatosis type 2 susceptibility protein | A1i | 2175-2400 |
| M13945 | Pim-1 proto-oncogene | A4a | 2713-2930 |
| M20157 | Egr-1 Zn-finger regulatory protein | D2i | 399-753 |
| M25811 | PKC-alpha; protein kinase C alpha type | B6e | 1566-1924 |
| M27129 | CD44 antigen | E6e | 789-1141 |
| M31042 | T-lymphocyte activated protein | D6h | 285-606 |
| M31131 | Neuronal-cadherin (N-cadherin) | E7k | 1212-1409 |
| M38700 | ATP-dependent DNA helicase II 70 kDa subunit; thyroid Ku (p70/p80) autoantigen p70 subunit; p70 Ku) | C5h | 274-632 |
| M63660 | G13; G-alpha-13 guanine nucleotide regulatory protein | B6n | 2057-2377 |
| M83380 | Transcription factor RelB | D7c | 1456-1728 |
| M84487 | Vascular cell adhesion protein 1 | E7m | 984-1304 |
| S71186 | ERCC3 DNA repair helicase; DNA-repair protein complementing XP-B cells (XPBC) | C6e | 1147-1444 |
| S76657 | CRE-BP1; cAMP response element binding protein 1 | B3l | 412-748 |
| U02887 | XRCC1 DNA-repair protein, affecting ligation | C7n | 900-1183 |
| U53228 | Nuclear hormone receptor ROR-ALPHA-1 | D5i | 368-675 |
| U57311 | 14-3-3 protein eta | B7g | 374-640 |
| X56135 | Prothymosin alpha | A7m | 186-455 |
| X57487 | PAX-8 (paired box protein PAX 8) | D5l | 680-1011 |
| X58995 | CamK IV; Ca2/calmodulin-dependent protein kinase IV (catalytic chain) | B5f | 1269-1608 |
| X66323 | ATP-dependent DNA helicase II 80 kDa subunit; thyroid Ku (p70/p80) autoantigen p80 subunit; p80 Ku) | C5i | 565-875 |
| X67812 | Ret proto-oncogene (Papillary thyroid carcinoma-encoded protein) | A4f | 2359-2580 |
| X68193 | Nm23-M2; nucleoside diphosphate kinase B; metastasis-reducing protein; c-myc-related transcription factor | C4c | 80-454 |

TABLE 2 (CONT)

| GenBank # | Gene Name | Array Coordinate | Position |
|-----------|--|------------------|-----------|
| X97052 | MAPKK6; MAP kinase kinase 6(dual specificity) (MKK6) | B6d | 375-711 |
| D17384 | DNA polymerase alpha catalytic subunit (p180) | C5i | 563-908 |
| D28492 | Caspase-3; Nedd2 cysteine protease (positive regulator of programmed cell death ICH-1 homologue) | C1b | 398-694 |
| D50621 | PSD-95/SAP90A | D6d | 1512-1889 |
| J04946 | Angiotensin-converting enzyme (ACE) (clone ACE.5.) | F6i | 850-1113 |
| L08235 | Clusterin; complement lysis inhibitor; testosterone-repressed prostate message 2; apolipoprotein J; sulfated glycoprotein-2 | C3b | 515-744 |
| L12721 | Adipocyte differentiation-associated protein | D1c | 404-709 |
| L21671 | Epidermal growth factor receptor kinase substrate EPS8 | D2k | 1592-1873 |
| L33768 | Jak3 tyrosine-protein kinase; Janus kinase 3 | B5j | 3123-3426 |
| L33779 | Desmocollin 2 | E6i | 1317-1691 |
| L47650 | Stat6; signal transducer and activator of transcription 6; IL-4 Stat; STA6 | B4g | 2057-2411 |
| M12056 | Lymphocyte-specific tyrosine-protein kinase LCK | A5a | 1205-1488 |
| M22115 | ERA-1 Protein (ERA-1-993) | D2i | 723-1062 |
| M26283 | Homeo Box protein 2.1 (Hox-2.1) | D4a | 647-884 |
| M32309 | Zinc finger X-chromosomal protein (ZFX) | D7n | 2153-2554 |
| M55512 | WT1; Wilms tumor protein; tumor suppressor | A2c | 1262-1563 |
| M57422 | Tristetraprolin | B4k | 262-504 |
| M96823 | Nucleobindin | D5j | 80-357 |
| M97013 | PAX-5 (B cell specific transcription factor) | D6a | 286-629 |
| S69336 | IFNGR2; interferon-gamma receptor second (beta) chain; interferon gamma receptor accessory factor-1 (AF-1) | B3b | 832-1089 |
| S74227 | Transcriptional enhancer factor 1 (TEF-1) | D7i | 934-1233 |
| U02079 | Transcription factor NFAT 1, isoform alpha | D7a | 1601-1910 |
| U05252 | DNA-binding protein SATB1 | D2e | 1101-1380 |
| U20372 | CCHB3; calcium channel (voltage-gated; dihydropyridine-sensitive; L-type) beta-3 subunit) | B2c | 351-639 |
| U20553 | p57kip2; cdk-inhibitor kip2 (cyclin-dependent kinase inhibitor 1B) member of the p21CIP1 Cdk inhibitor family; candidate tumor suppressor gene | A7g | 989-1272 |
| U36203 | snoN; ski-related oncogene | E2j | 671-1006 |
| X14759 | Homeo Box protein 7.1 (Hox-7.1) | D4f | 740-992 |
| X14943 | Neuronal cell surface protein F3 | E7i | 1033-1311 |
| X55123 | GATA-3 transcription factor | D3f | 858-1125 |

TABLE 2 (CONT)

| GenBank # | Gene Name | Array Coordinate | Position |
|-----------|---|------------------|-----------|
| X57621 | YB1 DNA binding protein | D7j | 550-873 |
| X58384 | Dipeptidyl peptidase iv | E7i | 61-294 |
| X59421 | Fli-1 eis-related proto-oncogene | A3b | 267-623 |
| X66224 | RXR-beta cis-11-retinoic acid receptor | B4c | 1225-1477 |
| X78445 | C3H cytochrome P450; Cyp1b1 | B1j | 295-593 |
| X96859 | Ubiquitin-conjugating enzyme, yeast Rad6 homologue; murine HR6B | C7k | 51-392 |
| Z27088 | Relaxin | C4i | 51-365 |
| Z27410 | Transcription factor LIM-1 | D6m | 1673-1934 |
| D10061 | DNA topoisomerase I (Top I) | C5m | 1051-1357 |
| D12513 | DNA topoisomerase II (Top II) | C5n | 520-870 |
| D30687 | GST Pi 1; glutathione S-transferase Pi 1; preadipocyte growth factor | C2d | 62-369 |
| J03958 | Glutathione S-transferase A | C1n | 54-311 |
| J04696 | Glutathione S-transferase Mu 1 | C2b | 13-263 |
| L10656 | c-Abl proto-oncogene | A4k | 878-1145 |
| M13071 | A-Raf proto-oncogene | A3k | 1042-1320 |
| M17031 | c-Src proto-oncogene | A4n | 452-758 |
| M35523 | Retinoic acid binding protein II cellular (CRABP-II) | D6e | 276-571 |
| M83749 | Cyclin D2 (G1/S-specific) | A6g | 781-1074 |
| U43844 | Cyclin D3 (G1/S-specific) | A6h | 484-790 |
| S49542 | 5-Hydroxytryptamine receptor [Serotonin receptor type 2 (5HT2)] | E4e | 400-707 |
| S78355 | Cyclin D1 (G1/S-specific) | A6f | 1858-2205 |
| U02098 | Pur-alpha transcriptional activator; sequence-specific ssDNA-binding protein | C7e | 1082-1309 |
| U27323 | Cdc25a; cdc25M1; MP11 (M-phase inducer phosphatase 1) | A7j | 606-986 |
| X07414 | ERCC-1; DNA excision repair protein | C6d | 189-484 |
| X15842 | c-rel proto-oncogene | A2m | 1729-2084 |
| X69618 | Inhibin alpha subunit | F2g | 810-1117 |
| X76341 | Glutathione reductase | C1m | 115-377 |
| X81581 | Insulin-like growth factor binding protein-3 (IGFBP-3) | F2k | 474-719 |
| Z26580 | Cyclin A (G2/M-specific) | A6a | 701-1009 |
| Z46845 | Preproglucagon | A5i | 172-531 |
| M61909 | NF-kB p65; NF-kappa-B transcription factor p65 subunit; rel-related polypeptide | B4a | 101-363 |
| D11091 | PKC-theta; protein kinase C theta type | B6h | 658-957 |
| D13867 | VLA-3 alpha subunit | E7n | 288-589 |

TABLE 2 (CONT)

| GenBank # | Gene Name | Array Coordinate | Position |
|-----------|--|------------------|-----------|
| D17571 | NADPH-cytochrome P450 reductase | C4a | 326-605 |
| D17584 | Beta-prolactykinin a | A5j | 273-523 |
| D30743 | Wee1/p87: cdc2 tyrosine 15-kinase | A7h | 1816-2159 |
| D83966 | Protein tyrosine phosphatase | C4g | 1060-1429 |
| J05205 | Jun-D; c-jun-related transcription factor | A3g | 737-964 |
| L23423 | Integrin alpha 7 | E7e | 2399-2713 |
| L28177 | Gadd45; growth arrest and DNA-damage-inducible protein | C3j | 144-434 |
| L35049 | Bcl-xL apoptosis regulator (bcl-x long); Bcl-2 family member | C1j | 641-906 |
| X03919 | N-myc proto-oncogene protein | A3j | 3262-3450 |
| M20473 | cAMP-dependent protein kinase type I-beta regulatory chain | B5g | 538-750 |
| M21065 | IRF1; interferon regulatory factor 1 | B7k | 1-233 |
| M36830 | HSP86; heat shock 86kD protein | B1d | 255-551 |
| M60778 | LFA1-alpha; integrin alpha L; leukocyte adhesion glycoprotein LFA-1 alpha chain; antigen CD11A (p180) | B3e | 1838-2050 |
| M88127 | APC; Adenomatous Polyposis Coli protein | A1a | 4127-4476 |
| S93521 | Cdc25b; cdc25M2; MPI2 (M-phase inducer phosphatase 2) | A7k | 1893-2200 |
| U03279 | PI3-K p110; phosphatidylinositol 3-kinase catalytic subunit | B6j | 1437-1723 |
| U03560 | HSP27; heat shock 27kD protein 1 | B1a | 245-500 |
| U05247 | Csk; c-Src-kinase and negative regulator | B4n | 645-984 |
| U06948 | Fas; Fas antigen ligand; generalized lymphoproliferation disease gene (gld) in mice | C3g | 168-488 |
| U10871 | MAPK; MAP kinase; p38 | B5m | 465-780 |
| U19597 | p19ink4; cdk4 and cdk6 inhibitor | A7d | 228-516 |
| U19617 | Elf-1 Ets family transcription factor | D2j | 1585-1902 |
| U21050 | CRAF1; TNF receptor (CD40 receptor) associated factor; TRAF-related | C3c | 1225-1466 |
| U25844 | SPI3; serpin; similar to human proteinase inhibitor 6 (placental thrombin inhibitor) serine proteinase inhibitor | C4l | 915-1230 |
| U25995 | RIP cell death protein; Fas/APO-1 (CD95) interactor, contains death domain | C4j | 1945-2223 |
| U29056 | SLAP; src-like adapter protein; Eck receptor tyrosine kinase-associated | B5c | 109-427 |
| U43678 | Atm; ataxia telangiectasia murine homologue | C5g | 8989-9170 |
| U51196 | EB1 APC-binding protein | A1e | 607-834 |
| U51907 | TANK; I-TRAF; TRAF family member associated NF-kB activator | B4h | 135-437 |

TABLE 2 (CONT)

| GenBank # | Gene Name | Array Coordinate | Position |
|-----------|--|------------------|-----------|
| U59463 | Caspase-11; ICH-3 cysteine protease; upstream regulator of ICE | C1a | 352-686 |
| U59883 | MLH1 DNA mismatch repair protein; MutL homologue | C6k | 1037-1278 |
| X04480 | Insulin-like growth factor-IA | F3a | 183-406 |
| X07640 | Cell surface glycoprotein MAC-1 alpha subunit | E6j | 1892-2179 |
| X13664 | N-ras proto-oncogene; transforming G-protein | A5e | 548-857 |
| X13945 | L-myc proto-oncogene protein | A3h | 5287-5590 |
| X14951 | CD18 antigen beta subunit (leukocyte adhesion LFA-1) (CD3, P150, 95) | E5n | 1366-1706 |
| X52191 | c-Fgr proto-oncogene | A4m | 1305-1538 |
| X53176 | Integrin alpha 4 | E7b | 2176-2449 |
| X53532 | PKC-beta; protein kinase C beta-II type | B6l | 1712-2089 |
| X53584 | HSP60; heat shock 60 kDa protein 1 (chaperonin, GroEL homologue); | B1b | 1432-1459 |
| X57111 | mitochondrial matrix protein P1 | A5b | 858-1151 |
| X59868 | c-Cbl proto-oncogene (Adaptor protein) | A7i | 942-1276 |
| | Cdc25 phosphatase; guanine nucleotide releasing protein | | |
| | Ezrin; Villin 2; NF-2 (merlin) related filament/plasma membrane associated protein | A1f | 1571-1812 |
| X60671 | | A6c | 1184-1447 |
| X64713 | Cyclin B1 (G2/M-specific) | E7d | 261-611 |
| X69902 | Integrin alpha 6 | E4j | 1422-1711 |
| X72395 | 5-Hydroxytryptamine (serotonin) receptor 3 | D4h | 141-362 |
| X73573 | Homeobox protein HOXD-3 | A6i | 799-1140 |
| X75888 | Cyclin E (G1/S-specific) | B5n | 719-987 |
| X76850 | MAPKAPK-2; MAP kinase-activated protein kinase; MAPKAP kinase 2 | A3d | 617-844 |
| X83971 | Fra-2 (fos-related antigen 2) | A6b | 656-916 |
| X84311 | Cyclin A1 (G2/M-specific) | | |
| | DCC; netrin receptor; immunoglobulin gene superfamily member; former tumor suppressor protein candidate | A1d | 4193-4508 |
| X85788 | | | |
| | MHR23A; Rad23 UV excision repair protein homologue; xeroderma pigmentosum group C (XPC) repair complementing protein | C6i | 613-955 |
| X92410 | | | |
| | MHR23B; Rad23 UV excision repair protein homologue; xeroderma pigmentosum group C (XPC) repair complementing protein | C6j | 542-807 |
| X92411 | | E7g | 1990-2320 |
| Y00769 | Integrin beta | C6n | 159-417 |
| Z32767 | MmRad52; yeast DNA repair protein Rad52 homologue | A6k | 300-619 |
| Z37110 | Cyclin G (G2/M-specific) | B3f | 1146-1442 |
| D13458 | Prostaglandin E2 receptor EP4 subtype | E3f | 1389-1739 |
| D90205 | Interleukin-5 receptor | | |

TABLE 2 (CONT)

| GenBank # | Gene Name | Array Coordinate | Position |
|-----------|---|------------------|-----------|
| J00380 | Epidermal growth factor (EGF) | F1j | 180-505 |
| J04843 | Erythropoietin receptor | E2a | 1193-1377 |
| J05149 | Insulin receptor | E4a | 653-1011 |
| K01700 | p53; tumor suppressor; DNA-binding protein | A1l | 1125-1517 |
| L03529 | Cf2r; coagulation factor II (thrombin) receptor | B2j | 762-1154 |
| L09562 | PTPRG; protein-tyrosine phosphatase gamma | B7l | 1248-1504 |
| L10075 | DNA-binding protein SMBP2 | D2f | 4790-5088 |
| L12120 | Interleukin-10 receptor | E3a | 1762-2110 |
| L20048 | Interleukin-2 receptor gamma chain | E3c | 1073-1313 |
| L24755 | Bone morphogenetic protein 1 | F1b | 2402-2676 |
| L33406 | Uromodulin | F4i | 1809-2136 |
| L34169 | Thrombopoietin | F4e | 652-954 |
| M13177 | Transforming growth factor beta | F4f | 772-1075 |
| M13926 | Granulocyte colony-stimulating factor (G-CSF) | F2a | 86-377 |
| M14220 | Neuroleukin | F3m | 1110-1490 |
| M14951 | Insulin-like growth factor-2 (somatomedin A) | F2n | 46-328 |
| M15131 | Interleukin 1 beta | F4k | 827-1225 |
| M16449 | c-myc proto-oncogene protein | A2k | 1212-1513 |
| M16819 | Tumor necrosis factor beta TNF-beta (Lymphotoxin-alpha) | F4h | 461-805 |
| M20658 | Interleukin-1 receptor | C3n | 2050-2410 |
| X05010 | CSF-1; M-CSF; colony stimulating factor-1 | A5g | 1268-1657 |
| M27959 | Interleukin-4 receptor (membrane-bound form) | E3e | 2469-2705 |
| M28233 | Interferon-gamma receptor | E2m | 1262-1550 |
| M29697 | Interleukin-7 receptor | E3g | 701-1104 |
| M34815 | Gamma interferon induced monokine (MIG) | F1m | 42-323 |
| M37897 | Interleukin 10 | F4l | 175-456 |
| M57999 | NF-kappa B binding subunit (nuclear factor) (TFDB5) | D5g | 3122-3417 |
| M59378 | Tumor necrosis factor receptor 1; TNFR-1 | C5d | 1961-2376 |
| M84607 | PDGFRa; platelet-derived growth factor alpha-receptor | A4e | 474-803 |
| M84746 | Interleukin-9 receptor | E3i | 795-1086 |
| M87039 | iNOS; nitric oxide synthase (inducible) | C3m | 3178-3455 |
| M89641 | Interferon alpha-beta receptor | E2l | 808-1120 |
| M94087 | Activating transcription factor 4 (mATF4) | D1b | 416-769 |
| S56660 | Beta2-FAR; retinoic acid receptor beta-2 | B3k | 589-896 |
| S67051 | Tie-2 proto-oncogene | A4l | 1843-2179 |

TABLE 2 (CONT)

| GenBank # | Gene Name | Array Coordinate | Position |
|-----------|---|------------------|-----------|
| U00182 | IGF-I-R alpha; insulin-like growth factor I receptor alpha subunit | C3i | 489-885 |
| U04710 | IGFR II; insulin-like growth factor receptor II, cation-independent mannose-6-P receptor; elevated in Wilms's tumor cells | C3k | 707-1060 |
| U06922 | Stat3; APRF; acute phase response factor | B4e | 1575-1910 |
| U18542 | Calcitonin receptor 1b | E3k | 1375-1630 |
| U32329 | Endothelin b receptor [Ednrb] | E1i | 279-695 |
| U32330 | Prepro-endothelin-3 | F4c | 703-1008 |
| X04367 | Pre-platelet-derived growth factor receptor | E2i | 2336-2677 |
| X04836 | CD 4 receptor (T cell activation antigen) | E1e | 1652-1877 |
| X07962 | Interleukin 7 | F5d | 241-496 |
| X12531 | Macrophage inflammatory protein | F3e | 25-359 |
| X14432 | Thrombomodulin | F4d | 1082-1365 |
| X51975 | Interleukin 6 (B cell differentiation factor) | F5c | 1638-1898 |
| X53779 | Androgen receptor | E3j | 2189-2491 |
| X56848 | Bone morphogenetic protein 4 (BMP-4) (TGF-beta family) | F1d | 1275-1513 |
| X57349 | Transferin receptor protein (p90, CD71) | B3h | 654-1023 |
| X57413 | Transforming growth factor beta 2 | F4g | 2227-2541 |
| X57497 | Glutamate receptor, ionotropic AMPA 1 | E5h | 1290-1657 |
| X57796 | TNF 55; tumor necrosis factor 1 (55kd) | C5b | 658-1022 |
| X58876 | Mdm2; p53-regulating protein | A1h | 1364-1646 |
| X61753 | Transcription factor 1 for heat shock gene | D6i | 203-570 |
| X65453 | CD40L; CD40 ligand | C2n | 545-809 |
| X68932 | c-Fms proto-oncogene (macrophage colony stimulating factor 1 (CSF-1) receptor) | A4b | 2399-2686 |
| X70472 | B-myb proto-oncogene; myb-related protein B | A2f | 2109-2456 |
| X76654 | Ear-2; v-erbA related proto-oncogene | A2n | 1065-1376 |
| X80764 | Tie-1 tyrosine-protein kinase receptor | B3g | 1425-1844 |
| D10651 | Glutamate receptor, ionotropic NMDA2B (epsilon 2) | E5j | 506-786 |
| D10217 | Glutamate receptor, ionotropic NMDA2A (epsilon 1) | E5i | 3966-4209 |
| D10329 | CD7 antigen | E6g | 28-421 |
| D00926 | Transcription factor S-II (transcription elongation factor) | D7d | 518-767 |
| D12482 | Basic Fibroblast growth factor (b- FGF) | F1a | 290-620 |
| D16250 | Bone morphogenetic protein receptor | E1c | 1454-1837 |
| D17292 | G-protein-coupled receptor | E2d | 833-1115 |
| D17407 | Transcription factor SP2 | D7g | 734-1079 |

TABLE 2 (CONT)

| GenBank # | Gene Name | Array Coordinate | Position |
|-----------|--|------------------|-----------|
| D29678 | Cdk5; cyclin-dependent kinase 5 | A6n | 552-882 |
| D25540 | TGF-beta receptor type 1 | E2k | 1407-1629 |
| D26077 | Kinesin like protein KIF 3B | F6a | 3519-3722 |
| D29951 | Kinesin family protein KIF1A | F5m | 2553-2830 |
| D38258 | Fibroblast growth factor 9 | F1k | 91-379 |
| D83698 | Neuronal death protein | C4b | 627-805 |
| D84372 | Syp; SH-PTP2; adaptor protein tyrosine phosphatase | B5e | 1229-1543 |
| J03168 | Interferon regulatory factor 2 (IRF 2) | D4l | 718-976 |
| J02870 | Laminin receptor 1 | E7j | 368-675 |
| D90176 | NF-1B protein (transcription factor) | D5f | 452-791 |
| J03236 | Jun-B; c-jun-related transcription factor | A3f | 514-740 |
| J03520 | Tissue plasminogen activator | F7e | 622-1020 |
| J03770 | Homeo Box protein 4.2 (Hox-4.2) | D4e | 565-945 |
| J04113 | Nur77 early response protein; thyroid hormone (TR3) receptor | C4d | 825-1059 |
| J04103 | Ets-2 transcription factor | D3b | 917-1281 |
| J04115 | c-Jun proto-oncogene (transcription factor AP-1 component) | A2i | 951-1238 |
| J05609 | Serine protease inhibitor homolog J6 | F7l | 581-855 |
| K01759 | Nerve growth factor beta (beta-NGF) | F3l | 642-901 |
| L01640 | Cdk4; cyclin-dependent kinase 4 | A6m | 230-616 |
| K02582 | Acetylcholine receptor delta subunit | E4l | 1400-1655 |
| L02526 | MAPKK1; MAP kinase kinase 3 (dual specificity) (MKK1) | B6a | 1284-1583 |
| L04662 | GABA-A transporter 4 | E5g | 960-1341 |
| L04663 | GABA-A transporter 3 | E5f | 1010-1320 |
| L07297 | Vegfr1; Vascular endothelial growth factor receptor 1 / Fms-related tyrosine kinase 1 (Flt1) | A4j | 1144-1541 |
| L10084 | Adrenergic receptor, beta 1 | E4m | 404-772 |
| L25890 | Eph3 (Nuk) tyrosine-protein kinase receptor | B2k | 2255-2491 |
| L16953 | MTJ1; DnaJ-like heat-shock protein from mouse tumor | B1e | 1059-1384 |
| L19622 | TIMP-3 tissue inhibitor of metalloproteinases-3 | F7n | 274-592 |
| L24563 | Insulin receptor substrate-1 (IRS-1) | E4b | 1027-1304 |
| L13968 | YY1 (UCRBP) transcriptional factor | D7k | 1052-1292 |
| L28095 | Interleukin-converting enzyme (ICE) | F7a | 30-269 |
| L38847 | Hepatoma transmembrane kinase ligand | F2f | 927-1219 |
| L36179 | Voltage-gated sodium channel | B2f | 4179-4505 |
| L37296 | Bad; heterodimeric partner for Bcl-XL and Bcl-2; promotes cell death | C1d | 1079-1375 |

TABLE 2 (CONT)

| GenBank # | Gene Name | Array Coordinate | Position |
|-----------|--|------------------|-----------|
| L35236 | Jnk stress-activated protein kinase (SAPK) | B5k | 795-1032 |
| M11686 | Cytoskeletal epidermal keratin (18 human) | F5i | 473-773 |
| M11434 | Nerve growth factor alpha (alpha-NGF) | F3k | 294-494 |
| M10937 | Epidermal keratin (1 human) | F5k | 326-683 |
| M14537 | Nicotinic acetylcholine receptor | E5k | 1226-1568 |
| M14757 | MDR1; P-glycoprotein; multidrug resistance protein; efflux pump | B1g | 1500-1886 |
| M18934 | CD2 antigen | E6a | 354-602 |
| M17192 | Homeo Box protein 1.1 (Hox-1.1) | D3n | 466-723 |
| M19436 | Fetal myosin alkali light chain | F5i | 205-504 |
| M25892 | Interleukin 4 | F5b | 77-310 |
| M26391 | Rb; pp105; Retinoblastoma susceptibility-associated protein (tumor suppressor gene; cell cycle regulator) | A1m | 2036-2296 |
| M28489 | Rsk; ribosomal protein S6 kinase | B6i | 1191-1436 |
| M29464 | Pletelet- derived growth factor (A chain) (PDGF- A) | F4b | 152-425 |
| M28698 | Cytoskeletal epidermal keratin (19 human) | F5j | 194-500 |
| M29475 | RAG-1; V(D)J recombination activating protein | C7g | 2155-2404 |
| M29855 | Interleukin-3 receptor | E3d | 1975-2254 |
| M30642 | K-fibroblast growth factor | F3c | 309-577 |
| M34381 | Octamer binding transcription factor (Oct 3) | D5k | 774-999 |
| M33960 | Plasminogen activator inhibitor | F7h | 1096-1344 |
| M33158 | CD3 antigen, delta polypeptide | E6c | 73-361 |
| M34857 | Homeo Box protein 2.5 (Hox-2.5) | D4c | 11-277 |
| M36829 | HSP84; heat shock 84kD protein | B1c | 342-366 |
| M55617 | Mast cell protease (MMCp) - 4 | F7b | 634-992 |
| M61177 | Erk1; extracellular signal-regulated kinase 1; p44; Erk2 | B5h | 115-373 |
| M50651 | PI3-K p85; phosphatidylinositol 3-kinase regulatory subunit; phosphoprotein p85; PDGF signaling pathway member | B6k | 981-1260 |
| M58633 | p58/GTA; galactosyltransferase associated protein kinase (cdc2-related protein kinase) | A7b | 1022-1284 |
| M64086 | Serine protease inhibitor 2 (spi-2) | F7j | 1499-1754 |
| M64429 | B-Raf proto-oncogene | A3l | 1651-2036 |
| M68513 | Elk1 (Mek4; HEK) tyrosine-protein kinase receptor HEK | B2l | 2681-2915 |
| M64796 | RAG-2; V(D)J recombination activating protein | C7h | 671-944 |
| M84324 | Collagenase type IV | F6k | 696-1040 |
| M83336 | Interleukin-6 receptor beta chain; membrane glycoprotein gp130 | B3c | 1423-1741 |

TABLE 2 (CONT)

| GenBank # | Gene Name | Array Coordinate | Position |
|-----------|---|------------------|-----------|
| M76601 | Alpha cardiac myosin heavy chain | F5e | 2094-2391 |
| M84819 | Retinoic acid receptor RXR- gamma | D6f | 701-1082 |
| M85078 | Granulocyte-macrophage colony-stimulating factor receptor | E2e | 904-1289 |
| M86566 | GABA-A receptor alpha-1 subunit | E5d | 1251-1606 |
| M93428 | Endothelial ligand for L-selectin (GLYCAM 1) | F1i | 182-541 |
| M95633 | Integrin beta 7 subunit | E7h | 2142-2423 |
| U00478 | DNase I | C6c | 665-871 |
| U03184 | Cortactin; protein tyrosine kinase substrate | B7h | 426-653 |
| U05672 | Adenosine A2M2 receptor | C2g | 491-735 |
| U04674 | DNA ligase I | C5j | 1678-2054 |
| U05671 | Adenosine A1M receptor | C2f | 302-673 |
| U04443 | Non-muscle myosin light chain 3 | F6b | 84-370 |
| U06119 | Cathepsin H | F6i | 325-694 |
| U06924 | Stat1; signal transducer and activator of transcription | B4d | 1749-2104 |
| U09507 | p21/Cip1/Waf1; cdk-inhibitor protein 1 | A7e | 9-403 |
| U11822 | Cdk7; MO15; cyclin-dependent kinase 7 (homologue of Xenopus MO15 cdk-activating kinase) | A7a | 454-824 |
| U10440 | p27kip1; G1 cyclin-Cdk protein kinase inhibitor, p21-related | A7f | 270-454 |
| U10551 | Gem; induced, immediate early protein; Ras family member | B7a | 220-471 |
| U12570 | VHL; Von Hippel-Lindau tumor suppressor protein | A2b | 885-1111 |
| U12983 | Cek 5 receptor protein tyrosine kinase ligand | F1g | 1037-1287 |
| U13705 | Glutathione peroxidase (plasma protein); selenoprotein. | C1l | 766-1046 |
| U14135 | Integrin alpha 5 (CD51) | E7c | 2170-2516 |
| U14173 | Ski proto-oncogene | A4g | 707-1037 |
| U17698 | Abipilin-1 (abi-1) similar to HOXD3 | D1a | 351-585 |
| U17162 | BAG-1; bcl-2 binding protein with anti-cell death activity | C1e | 17-334 |
| U15784 | Shc transforming adaptor protein; Src homology 2 (SH2) protein, SHB-related | A5f | 1220-1451 |
| U18310 | MAPKK4; MAP kinase kinase 4; Jnk activating kinase 1; (JNKK1; SEK1; MKK4) | B6c | 1380-1749 |
| U19118 | Transcription factor LRG - 21 | D6n | 618-966 |
| U19119 | Interferon inducible protein 1 | D4k | 1342-1636 |
| U19463 | A20 zinc finger protein; apoptosis inhibitor | C2e | 1952-2293 |
| U19596 | p18ink4; cdk4 and cdk6 inhibitor | A7c | 16-284 |
| U19799 | I-kB (I-kappa B) beta | B3n | 419-778 |

TABLE 2 (CONT)

| GenBank # | Gene Name | Array Coordinate | Position |
|-----------|--|------------------|-----------|
| U24160 | Dvl2; dishevelled-2 tissue polarity protein | B7i | 1205-1578 |
| U20532 | Nuclear factor related to P45 NF-E2 | D5h | 1429-1759 |
| U21011 | MSH2 DNA mismatch repair protein; MutS homologue 2 | C7a | 2150-2490 |
| U20238 | GapIII; GTPase-activating protein | B7j | 328-644 |
| U25685 | Syk tyrosine-protein kinase (activated p21cdc42Hs kinase (ack)) | B5d | 1235-1524 |
| U27177 | p107; RBL1; Retinoblastoma gene product-related protein p107 (cell cycle regulator) | A1j | 1973-2365 |
| U28724 | PMS2 DNA mismatch repair protein; yeast PMS1 homologue 2 | C7d | 749-1013 |
| U29173 | Limphotoxin receptor (TNFR family) | E2g | 1415-1668 |
| U31625 | BRCA1; Breast/ovarian cancer susceptibility locus 1 product | A1b | 5126-5430 |
| U33626 | Pml; Murine homologue of the leukemia-associated PML gene | B4b | 1667-2064 |
| U34960 | Transducin beta-2 subunit | B7e | 515-834 |
| U36277 | I-kB (I-kappa B) alpha chain | B3m | 541-823 |
| U37522 | TRAIL; TNF-related apoptosis inducing ligand; Apo-2 ligand | C5c | 981-1288 |
| U36799 | p130; Retinoblastoma gene product-related protein Rb2/p130 (cell cycle regulator) | A1k | 970-1321 |
| U36340 | CACCC Box- binding protein BKLf | D1j | 826-1065 |
| U39643 | FAF1; Fas-associated protein factor, apoptosis activator | C3e | 423-681 |
| U41671 | Zinc finger transcription factor RU49 | D7m | 1229-1591 |
| U42190 | GTBP; G/T-mismatch binding protein; MSH6 | C6g | 1477-1769 |
| U43144 | PLC beta; phospholipase C beta 3 | B6i | 1933-2271 |
| U43205 | Frizzled-3; Drosophila tissue polarity gene frizzled homologue 3; dishevelled receptor | B2m | 2037-2285 |
| U43187 | MAPKK3; MAP kinase kinase 3 (dual specificity) (MKK3, MEK3) | B6b | 1436-1742 |
| U43525 | Myeloblastin; trypsin-chymotrypsin related serine protease | A7i | 503-807 |
| U47104 | Zinc finger Kruppel type Zip 92 | D7i | 578-896 |
| U44088 | TDAG51; couples TCR signaling to Fas (CD95) expression | C5a | 729-1042 |
| U43788 | POU domain, class 2, associated factor 1 | D6c | 610-884 |
| U48853 | Cas; Crk-associated substrate; focal adhesion kinase substrate | B4i | 1982-2216 |
| U49112 | ALG-2; calcium binding protein required for programmed cell death | C2i | 527-861 |
| U49739 | Unconventional myosin VI | F6e | 3784-4021 |
| U51037 | Transcription factor CTCF (11 zinc fingers) | D6i | 1625-1911 |
| U53925 | Transcription factor C 1 | D6k | 3895-4227 |

TABLE 2 (CONT)

| GenBank # | Gene Name | Array Coordinate | Position |
|-----------|--|------------------|-----------|
| U58992 | Madrl; mSmad1; Mothers against dpp protein (Mad) murine homologue; TGF-beta signaling protein-1 (bsp-1); candidate tumor suppressor gene | A1g | 238-476 |
| U59746 | Bcl-W apoptosis regulator; Bcl-2 family member | C1i | 153-368 |
| U60530 | Mad related protein 2 (MADR2) | F3h | 584-820 |
| U62638 | Cyclin C (G1-specific) | A6e | 714-986 |
| U63386 | Mph-1 nuclear transcriptional repressor for hox genes | D5a | 1621-1884 |
| U66887 | Rad50; DNA repair protein | C7i | 1383-1707 |
| U70324 | Fyn proto-oncogene; Src family member | B5a | 584-882 |
| X01023 | c-myc proto-oncogene protein | A2i | 379-667 |
| V00727 | c-Fos proto-oncogene; transcription factor AP-1 component. fos cellular oncogene | A2h | 482-734 |
| X06086 | Cathepsin L | F6j | 267-588 |
| X04648 | Glutamate receptor channel subunit gamma | E6n | 41-408 |
| X12616 | c-Fes proto-oncogene | A4i | 2342-2598 |
| X12822 | Cytotoxic cell protease 2 (B10) | F6i | 439-686 |
| X07439 | Homeo Box protein 3.1 (Hox-3.1) | D4d | 449-722 |
| X13721 | Homeo Box protein 2.4 (Hox-2.4) | D4b | 1949-2284 |
| X14897 | Fos-B; c-fos-related protein fos B | A3c | 920-1278 |
| X16490 | Plasminogen activator inhibitor-2 | F7i | 674-978 |
| X51983 | c-ErbA oncogene; thyroid hormone receptor. | A2g | 400-675 |
| X53337 | Cathepsin D | F6h | 587-894 |
| X51438 | Vimentin | F6d | 868-1096 |
| X53476 | HMG-14 non histone chromosomal protein | D3m | 643-1017 |
| X53798 | Macrophage inflammatory protein 2 alpha (MIP 2 alpha) | F3g | 14-352 |
| X56906 | Bone morphogenetic protein 7 (BMP-7) (osteogenic protein 1) | F1e | 670-971 |
| X56959 | Transcription factor SP1P (POUdomain transcription factor) | D7f | 866-1128 |
| X59252 | Homeo Box protein 8 (Hox-8) | D4g | 826-1132 |
| X59927 | Fibroblast growth factor receptor 4 | E2b | 2446-2820 |
| X57277 | Rac1 murine homologue | B7c | 425-651 |
| X60831 | Transcription factor UBF | D7h | 689-993 |
| X61435 | Kinesin heavy chain | F5n | 1898-2182 |
| X61800 | CCAAT- Binding transcription factor (C/EBP) | D1k | 904-1150 |
| X62622 | TIMP-2 tissue inhibitor of metalloproteinases-2 | F7m | 1236-1468 |
| X63190 | Ets-related protein PEA 3 | D3a | 1702-2040 |

TABLE 2 (CONT)

| GenBank # | Gene Name | Array Coordinate | Position |
|-----------|---|------------------|-----------|
| X64361 | Vav; GDP-GTP exchange factor; proto-oncogene | B7i | 1083-1351 |
| X63963 | PAX-6 (paired box protein) | D6b | 1081-1325 |
| X66032 | Cyclin B2 (G2/M-specific) | A6d | 874-1236 |
| X67083 | Chop10; murine homologue of Gadd153 (growth arrest and DNA-damage-inducible protein) | C3a | 17-332 |
| X67914 | PD-1 possible cell death inducer; Ig gene superfamily member | C4f | 1481-1734 |
| X69619 | Inhibin beta A subunit (TGF beta family) | F2h | 1064-1304 |
| X70842 | Vegfr2; KDR/tik1 vascular endothelial growth factor tyrosine kinase receptor | B3j | 1394-1721 |
| X70296 | Protease nexin 1 (PN-1) | F7d | 746-985 |
| X71327 | MRE-binding transcription factor | D5b | 552-916 |
| X72711 | Activator -1 140 KD subunit (replication factor C 140KD) | C5e | 4137-4375 |
| X72310 | DP-1 (DRTF-polipeptide 1) cell cycle regulatory transcription factor | D2g | 925-1305 |
| X72230 | 5-Hydroxytryptamine (serotonin) receptor 1c | E4g | 982-1314 |
| X72795 | Gelatinase B | F6n | 599-954 |
| X74351 | XPAC; xeroderma pigmentosum group A correcting protein | C7m | 447-669 |
| X75427 | Integrin alpha 2 (CD49b) | E7a | 1595-1976 |
| X77113 | Growth/ differentiation factor 2 (GDF-2) | F2c | 939-1329 |
| X81582 | Insulin-like growth factor binding protein-4 (IGFBP-4) | F2l | 781-1140 |
| X81579 | Insulin-like growth factor binding protein-1 (IGFBP-1) | F2j | 27-256 |
| X81580 | IGFBP-2; insulin-like growth factor binding protein 2; autocrine and/or paracrine growth promoter | A5m | 449-817 |
| X81583 | Insulin-like growth factor binding protein-5 (IGFBP-5) | F2m | 461-824 |
| X81584 | Insulin-like growth factor binding protein -6 (IGFBP 6) | F2l | 701-1039 |
| X82327 | A-myb proto-oncogene; myb-related protein A | A2e | 1017-1334 |
| X83536 | Membrane type matrix metalloproteinase | F7c | 877-1101 |
| X87257 | Elk-1 ets-related proto-oncogene | A3a | 1498-1680 |
| X86925 | E2F-5 transcription factor | D2h | 426-728 |
| X90829 | Lbx 1 transcription factor | D4n | 1000-1306 |
| X91144 | P-selectin (glycoprotein ligand-1) | E5l | 1095-1323 |
| X91753 | Transcription factor SEF2 | D7e | 755-1054 |
| Z11974 | Macrophage mannose receptor | E2h | 807-1197 |
| X95403 | Rab-2 ras-related protein | B7b | 232-505 |
| X98055 | Gluthathione S-transferase (theta type1); phase II conjugation enzyme | C2c | 14-298 |
| X99063 | Zyxin; LIM domain protein; alpha-actinin binding protein | B7n | 1437-1812 |

TABLE 2 (CONT)

| GenBank # | Gene Name | Array Coordinate | Position |
|-----------|--|------------------|-----------|
| Y00671 | Met protooncogene | A4d | 3646-3933 |
| Y00864 | c-Kit proto-oncogene (mast/stem cell growth factor receptor tyrosine kinase) | A4c | 2867-3181 |
| Y07960 | Transcription factor BARX1 (homeodomain transcription factor) | D6j | 723-973 |
| X95346 | PLC gamma; phospholipase C gamma | B6m | 180-516 |
| Z12604 | Stromelysin-3; matrix metalloproteinase-11 (MMP-11) | C4n | 1463-1806 |
| Z14224 | 5-Hydroxytryptamine (serotonin) receptor 1e beta | E4h | 530-774 |
| Z15119 | 5-Hydroxytryptamine (serotonin) receptor 2c | E4i | 588-940 |
| Z19521 | Low density lipoprotein receptor | E4d | 1047-1324 |
| Z23107 | 5-Hydroxytryptamine (serotonin) receptor 7 | E4k | 460-817 |
| Z22649 | c-Mpl; thrombopoietin receptor; hematopoietic growth factor receptor superfamily member | A5k | 1561-1772 |
| Z21848 | DNA-polymerase delta catalytic subunit | C6b | 1256-1600 |
| Z29532 | Follistatin | F1i | 764-1053 |
| Z47766 | Cyclin F (S/G2/M-specific) | A6j | 2431-2708 |
| Z36885 | Ets-related protein Sap 1A | D3c | 1267-1521 |
| Z32815 | Net; ets related transcription factor; activated by Ras | A3i | 1211-1595 |
| Z48538 | Stat5a; mammary gland factor | B4f | 2269-2628 |
| Z49086 | Hek2 murine homologue; Mdk5 mouse developmental kinase; Eph-related tyrosine-protein kinase receptor | B2n | 1702-1930 |
| D26177 | D-Factor/LIF receptor | E1i | 2376-2775 |
| M13806 | Cytoskeletal epidermal keratin (14 human) | F5h | 108-469 |
| M21019 | R-ras protein, closely related to ras proto-oncogenes | B7d | 215-555 |
| M22959 | Prolactin receptor PRLR2 | E4c | 1-328 |
| M30903 | Blk; B lymphocyte kinase; Src family member | C2j | 1307-1672 |
| M35590 | Macrophage inflammatory protein 1 beta (Act 2) | F3f | 119-445 |
| M75716 | Alpha-1 protease inhibitor 2 | F7g | 625-969 |
| M92378 | GABA-A transporter 1 | E5e | 1131-1416 |
| M97017 | Bone morphogenetic protein 8a (BMP-8a) (TGF-beta family) | F1i | 788-1139 |
| M97200 | Erythroid kruppel-like transcription factor | D2n | 783-1171 |
| M98339 | GATA binding transcription factor (GATA-4) | D3e | 81-379 |
| M98547 | Growth factor receptor | E2f | 1701-2014 |
| S72408 | Crk adaptor protein | B4m | 750-1027 |
| U09419 | Retinoid X receptor interacting protein (RIP 15) | D6g | 1388-1682 |
| U14752 | Cek 7 receptor protein tyrosine kinase ligand | F1h | 504-837 |

TABLE 2 (CONT)

| GenBank # | Gene Name | Array Coordinate | Position |
|-----------|---|------------------|-----------|
| U29678 | C-C CKR-1; CCR-1; C-C chemokine receptor type 1, macrophage inflammatory protein-1 alpha receptor; MIP-1alpha-R; RANTES-R | B2i | 168-495 |
| X13358 | Glucocorticoid receptor form A | E3m | 1527-1816 |
| X83106 | Mothers against DPP protein (mad homolog Smad 1, transforming growth factor beta signaling protein) | F3j | 464-728 |
| Y00487 | Hck tyrosine-protein kinase | B5b | 1308-1563 |
| AB000777 | Photolyase/blue-light receptor homologue | C7c | 1418-1737 |
| D49482 | Osp94 osmotic stress protein; APG-1; hsp70-related | B1f | 1026-1266 |
| D78645 | Glucose regulated protein, 78kD; Grp78 | B1m | 167-411 |
| D87747 | LCR-1; CXCR-4; CXCR-4 (SDF-1) chemokine receptor 4; HIV coreceptor (lusin); G protein-coupled receptor LCR1 homologue; | B3d | 584-867 |
| M23384 | Glucose transporter-1, erythrocyte; Glut1 | B2e | 325-653 |
| M80456 | Int-3 proto-oncogene; NOTCH family member; NOTCH4 | A5h | 1846-2145 |
| M94335 | c-Akt proto-oncogene; Rac-alpha; protein kinase B (PKB) | C2k | 604-899 |
| Y13231 | Bak apoptosis regulator; Bcl-2 family member | C1f | 1509-1786 |
| U57324 | PS-2; homologue of the Alzheimer's disease gene | C4h | 437-783 |
| U65594 | BRCA2; Breast cancer susceptibility locus 2 product | A1c | 649-922 |
| U66058 | DNA ligase III | C5k | 2980-3205 |
| U67321 | Caspase-7; Lice2; ICE-LAP3 cysteine protease | C1c | 1040-1280 |
| U75506 | BID; apoptic death agonist | C1k | 452-777 |
| U92456 | WBP6; pSK-SRPK1; WW domain binding protein 6 serine kinase for SR splicing factors | B7m | 482-774 |
| U95826 | Cyclin G2 (G2/M-specific) | A6l | 408-688 |
| X99018 | Ung1; uracil-DNA glycosylase | C7l | 444-729 |
| Y14019 | Rab-3b ras-related protein | F6c | 232-562 |
| U28423 | Inhibitor of the RNA-activated protein kinase, 58-kDa | B5i | 180-487 |
| U34259 | Golgi 4-transmembrane spanning transporter; MTP | B2d | 742-1060 |
| U34920 | ATP-binding cassette 8; ABC8; homolog of Drosophila white | B2b | 1011-1319 |
| U37720 | CDC42 GTP-binding protein; G25K | F5g | 1675-1982 |
| U41751 | Etoposide induced p53 responsive (EI24) mRNA | B1l | 1041-1296 |
| U51866 | Casein kinase II (alpha subunit) | A3n | 1237-1517 |
| U52945 | TSG101 tumor susceptibility protein | A1n | 446-713 |
| U54705 | Tumor suppressor maspin | A2a | 251-507 |
| U97076 | FLIP-L; apoptosis inhibitor; FLICE-like inhibitory protein | C3h | 1476-1811 |
| X63615 | CamK II; Ca2+/calmodulin-dependent protein kinase II (beta subunit) | F5f | 1951-2219 |

TABLE 2 (CONT)

| GenBank # | Gene Name | Array Coordinate | Position |
|--------------|---|------------------|-----------|
| Z49085 | Htk; Mdk2 mouse developmental kinase; Eph -related tyrosine-protein kinase receptor | B3a | 2032-2365 |
| D49921 | Glial cell line-derived neurotrophic factor | F1n | 236-539 |
| L06039 | CD31 (Platelet endothelial cell adhesion molecule 1) | E6d | 1172-1494 |
| L16928 | CD22 antigen | E6i | 2314-2645 |
| L39770 | Gbx 2 | D3g | 1122-1395 |
| M12302 | Cytotoxic T lymphocyte-specific serine protease CCP 1 gene (CTLA-1) | F6m | 585-830 |
| M14222 | Cathepsin B | F6g | 382-729 |
| M33324 | Growth hormone receptor | E3n | 1942-2240 |
| M34563 | CD28 (receptor for B71) | E6b | 544-774 |
| M38651 | Estrogen receptor | E3l | 742-1013 |
| S71251 | Monocyte chemoattractant protein 3 | E1k | 201-491 |
| U03856 | CD45 associated protein (CD 45-ap, LSM-1) | E6f | 620-898 |
| U11688 | Orphan receptor | E1b | 1686-1943 |
| U17985 | Cannabinoid receptor 1 (brain) | E4n | 1091-1437 |
| U43512 | Dystroglycan 1 | E6m | 2267-2505 |
| U46923 | G-protein coupled receptor | E5c | 350-671 |
| X02389 | Urokinase type plasminogen activator | F7l | 1301-1538 |
| X05719 | CTLA-4 (immunoglobulin superfamily member) | E6k | 246-519 |
| X56182 | Myogenic factor 5 | D5d | 232-528 |
| X62700 | uPAR1; urokinase plasminogen activator surface receptor (CD87) | B3i | 482-756 |
| X69832 | Serine protease inhibitor 2.4 | F7k | 621-927 |
| X70298 | SRY-box containing gene 4 | D7b | 34-311 |
| L25602 | Bone morphogenetic protein 2 (BMP-2) (TGF-beta family) | F1c | 8372-8724 |
| M10021 [K02] | [K02588] P-1-450; dioxin-inducible cytochrome P450 | B2a | 3729-4014 |
| M16506 | Bcl-2; B cell lymphoma protein 2, apoptosis inhibitor | C1h | 2125-2367 |
| M34510 | CD14 antigen | E6h | 667-931 |
| M81832 | Somatostatin receptor 2 | E3b | 47-310 |
| U19880 | Dopamine receptor 4 | E5b | 907-1191 |
| U21681 | Cannabinoid receptor 2 (macrophage, CB2) | E5a | 910-1262 |
| U58533 | Erf (Ets-related transcription factor) | D2m | 1286-1613 |
| Z11597 | 5-Hydroxytryptamine (serotonin) receptor 1b | E4f | 1043-1355 |
| D78382 | Tob antiproliferative factor; interacts with p185erbB2 | A7n | 540-876 |
| J03752 | Glutathione S-transferase (microsomal) | C2a | 185-428 |
| L20331 | Adenosine A3 receptor | C2h | 182-382 |

TABLE 2 (CONT)

| GenBank # | Gene Name | Array Coordinate | Position |
|-----------|--|------------------|------------|
| U05341 | p55cdc; cell division control protein 20 | C4e | 1061-1348 |
| U12273 | AP endonuclease; apurinic/apyrimidinic endonuclease (Apex) | C5f | 1894-2150 |
| X67735 | Mas proto-oncogene (G-protein coupled receptor) | A5i | 566-808 |
| D26046 | AT motif-binding factor ATBF1 | D1d | 9807-10112 |
| D49474 | HMG-box transcription factor from testis (MusSox17) | D3i | 427-662 |
| L03547 | Ikaros DNA binding protein | D4i | 627-890 |
| L12147 | Early B cell factor (EBF) | D2a | 750-1026 |
| L12703 | Engrailed protein (En-1) homolog | D2b | 1323-1554 |
| L12705 | Engrailed protein (En-2) homolog | D2c | 1626-1895 |
| L21027 | Transcription factor A10 | B4i | 499-806 |
| L26507 | Myocyte nuclear factor (MNF) | D5c | 1203-1456 |
| L36435 | Basic domain/leucine zipper transcription factor | D1e | 872-1073 |
| M37163 | Caudal type Homeobox 1 (Cdx1) | D1i | 1040-1301 |
| M58566 | Butyrate response factor 1 | D1i | 768-1054 |
| S53744 | Brain specific transcription factor NURR-1 | D1g | 1548-1754 |
| S68377 | Bm-3.2 POU transcription factor | D1h | 877-1237 |
| S74520 | Caudal type Homeobox 2 (Cdx2) | D1m | 1085-1367 |
| U01036 | Erythroid transcription factor NF-E2 | D2d | 1-241 |
| U20344 | Gut-specific Kruppel-like factor GKLF | D3i | 1558-1789 |
| U25096 | Kruppel-like factor LKLF | D4m | 898-1193 |
| U29086 | Neuronal helix-loop-helix protein NEX-1 | D5e | 572-907 |
| U36760 | Brain factor 1 (Hfbbf1) | D1f | 1080-1318 |
| U41626 | Split hand/foot gene | D5m | 92-303 |
| U42554 | Sim transcription factor | D1n | 2828-3066 |
| U59876 | Glial cells missing gene homolog (mGCM1) | D3h | 727-1080 |
| U62522 | Sp4 zinc finger transcription factor | D4j | 1704-1929 |
| X61754 | Heat shock transcription factor 2 (HSF 2) | D3j | 1445-1640 |
| X83974 | RNA polymerase I termination factor TTF-1 | A2j | 3222-3433 |
| L35949 | Hepatocyte nuclear factor 3/forkhead homolog 8 (HFH-8) | D3k | 913-1232 |
| X94125 | SRY-box containing gene 3 (Sox3) | D5n | 212-443 |
| D13759 | Cot proto-oncogene | A3m | 696-956 |
| D49429 | HR23spA; protein involved in DNA double-strand break repair; PW29; calcium-binding protein | C6h | 103-434 |
| D64107 | Mmlim15; RecA-like gene; DMC1 homologue; meiosis-specific homologous recombination protein | C6i | 581-781 |

TABLE 2 (CONT)

| GenBank # | Gene Name | Array Coordinate | Position |
|-----------|---|------------------|-----------|
| J05186 | ERp72 endoplasmic reticulum stress protein; protein disulfide isomerase-related protein | B1k | 1160-1470 |
| S50213 | HMG1-related VDJ recombination signal binding protein | B1h | 2263-2531 |
| S65038 | Gli oncogene; zinc finger transcription factor | A3e | 104-505 |
| U05245 | Tiam-1 invasion inducing protein; GDP-GTP exchanger-related | A5n | 4329-4628 |
| U16805 | Sik; Src-related intestinal kinase | C4k | 1246-1623 |
| U28495 | Lfc proto-oncogene | A5d | 853-1150 |
| U40930 | Oxidative stress-induced protein mRNA | B1n | 1248-1561 |
| U43900 | STAM; signal transducing adaptor molecule | C4m | 576-811 |
| U46854 | ShcC adaptor; Shc-related; brain-specific | C7i | 246-601 |
| U58987 | Mmmre11a putative endo/exonuclease | B1i | 866-1204 |
| X53068 | PCNA; proliferating cell nuclear antigen; processivity factor | C7b | 53-320 |
| X81464 | Translin; recombination hotspot binding protein | C7j | 205-431 |
| X96618 | PA6 stromal protein; RAG1 gene activator | C6a | 442-749 |
| U18342 | Sky proto-oncogene (Tyr03; Rse; Dtk) | A4h | 1927-2286 |
| Z50013 | H-ras proto-oncogene; transforming G-protein | A5c | 1307-1544 |
| L47239 | ERBB-2 receptor (c-neu, HER2 protein tyrosine kinase) | E1m | 16-42 |
| L47240 | ERBB-3 receptor | E1n | 4-243 |
| U22516 | Placental ribonuclease inhibitor (Angiogenin) | F4a | 512-766 |
| L00923 | myosin I | G13 | 2578-2921 |
| U459777 | Ca2+ binding protein, Cab45 | G20 | 597-1082 |
| M10624 | murine ornithine decarboxylase | G14 | 865-1252 |
| X51703 | ubiquitin | G5 | 123-547 |
| J00423 | Hypoxanthine-guanine phosphoribosyltransferase | G7 | 301-751 |
| D78647 | phospholipase A2 | G6 | 446-813 |
| L31609 | ribosomal protein S29 | G21 | 5-244 |
| M325999 | glyceraldehyde-3-phosphate dehydrogenase | G12 | 765-1016 |
| M12481 | beta-actin | G19 | 25-564 |

Cancer Array

In the cancer arrays of the subject invention, the polynucleotide probe compositions on the array correspond to those genes which are associated, e.g. play a role in, cellular proliferative diseases, particularly cancer, where human genes are of particular interest in many embodiments. Types of genes that are typically represented on a cancer array of the subject invention include: oncogenes, tumor suppressors, cell cycle regulators, genome plasticity genes, apoptosis genes, cell differentiation genes, regulators of tumor host interaction and metastasis, such as extracellular matrix proteins, cell adhesion receptors, molecules that control cell invasion and motility, and genes associated with angiogenesis.

10 In certain embodiments, of particular interest is an array having the following types of genes represented on its surface: cell cycle/growth regulators; apoptosis; growth factors/cytokines; oncogenes/tumor suppressors; cell adhesion, motility and invasion; invasion regulators; GTP ases and their regulators; cadherins; intermediate filament markers; receptors; cell fate/development regulators; DNA damage/response/repair/ recombination; 15 and angiogenesis regulators. In a specific cancer array of interest, the spots are as listed in Table 3.

The cancer array finds use in a variety of applications, including: monitoring cellular responses to therapeutic compounds; comparing expression profiles of tumors at different developmental stages; developing diagnostic tools for distinguishing closely related tumors; 20 and the like.

In the following Table 3, as well as preceding Tables 1 and 2, the "position" coordinate refers to the actual nucleotide residues of the listed gene that are represented on the array.

TABLE 3

| Cell Cycle/Growth Regulators | GenBank # | Array Coordinate | Position |
|--|------------------|------------------|-----------|
| QUADRANT A | | | |
| CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.1-) (P34 PROTEIN KINASE) (CYCLIN-DEPENDENT KINASE 1) (CDK1) | X05360 | A1a | 655-886 |
| CELL DIVISION PROTEIN KINASE 2 (EC 2.7.1.1-) (P33 PROTEIN KINASE) | M68520 | A1b | 1774-2180 |
| CELL DIVISION PROTEIN KINASE 3 (EC 2.7.1.1-) | X66357 | A1c | 216-882 |
| CELL DIVISION PROTEIN KINASE 4 (EC 2.7.1.1-) (PSK-J3) | M14505 | A1d | 372-693 |
| CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.1-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE). | X66364 | A1e | 468-767 |
| CELL DIVISION PROTEIN KINASE 6 (EC 2.7.1.1-) (KINASE PLSTIRE) | X66365 | A1f | 315-663 |
| CELL DIVISION PROTEIN KINASE 7 (EC 2.7.1.1-) (CDK-ACTIVATING KINASE) (CAK) (39 KD PROTEIN KINASE) (P39 MO15) (STK1) (CAK1). | L20320 | A1g | 89-305 |
| CYCLIN-DEPENDENT KINASE 5 ACTIVATOR ISOFORM P39I | U34051 | A1h | 763-1-62 |
| PRECURSOR (CDK5 ACTIVATOR) (P39I). | X80343 | | |
| CYCLIN-DEPENDENT KINASE 5 ACTIVATOR PRECURSOR (CDK5 ACTIVATOR) (TAU PROTEIN KINASE II 23 KD SUBUNIT) (TPKII REGULATORY SUBUNIT) (P23) (P25) (P35). | M81933 | A1i | 551-941 |
| cdc25A; M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) | M81934; [S78187] | A1j | 1632-1978 |
| cdc25B; M-PHASE INDUCER PHOSPHATASE 2 (EC 3.1.3.48). | | A1k | 2286-2602 |
| [CDC25Hu2] | M34065 | A1l | 331-623 |
| cdc25C; M-PHASE INDUCER PHOSPHATASE 3 (EC 3.1.3.48). | L29222 | A1m | 144-459 |
| CLK-1 | L29216 | A1n | 1106-1356 |
| CLK-2 | L29220 | A2a | 551-1002 |
| CLK-3 | X66358 | A2b | 276-461 |
| SERINE/THREONINE-PROTEIN KINASE KIALRE | X66363 | A2c | 1114-1434 |
| SERINE/THREONINE-PROTEIN KINASE PCTAIRE-1 | X66360 | A2d | 954-1250 |
| SERINE/THREONINE-PROTEIN KINASE PCTAIRE-2 | X66362 | A2e | 549-911 |
| SERINE/THREONINE-PROTEIN KINASE PCTAIRE-3 | L25676 | A2f | 367-635 |
| SERINE/THREONINE-PROTEIN KINASE PITALRE | M80629 | A2g | 1388-1548 |
| CDC2-RELATED PROTEIN KINASE CHED | L33264 | A2h | 454-755 |
| CDC2-RELATED KINASE PISSLRE | X51688 | A2i | 876-1218 |
| CYCLIN A | M25753 | A2j | 979-1311 |
| CYCLIN B1 G2/MITOTIC-SPECIFIC | M74091 | A2k | 6670-7326 |
| CYCLIN C G1/S-SPECIFIC | X59798; [M64349] | A2l | 3427-3784 |
| CYCLIN D1 (CYCLIN PRAD1) (BCL-1 ONCOGENE) | D13639 [M90813] | A2m | 3932-4284 |
| CYCLIN D2 | M92287 | A2n | 537-894 |
| CYCLIN D3 | | | |

TABLE 3 (CONT)

| Cell Cycle/Growth Regulators | GenBank # | Array Coordinate | Position |
|---|------------------|------------------|-----------|
| CYCLIN E | M73812 | A3a | 1295-1658 |
| CYCLIN G1 | U47413 [L49504] | A3b | 755-1035 |
| CYCLIN G2 | U47414 [L49506] | A3c | 989-1254 |
| CYCLIN H | U11791 [U12685] | A3d | 717-1026 |
| CYCLIN-DEPENDENT KINASE INHIBITOR 1 (MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN 6) (MDA-6) (P21) (CDK-INTERACTING PROTEIN 1) (CIP1) (WAF1) (CDKN1A) (CDKN1) (SDI1) (PIC1) (CAP20) | U09579; [L25610] | | |
| CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITOR P57) (P57KIP2) | U22398 | A3e | 1745-2063 |
| CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). (CDKN2A) | L27211 | A3f | 1048-1316 |
| CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B) (MULTIPLE TUMOR SUPPRESSOR 2) (MTS2) (CDKN2B). | U17075; [L36844] | A3g | 482-836 |
| CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D). | U40343; [U20498] | A3h | 116-462 |
| WEE1-LIKE PROTEIN KINASE (EC 2.7.1.112) (Wee1Hu) | U10564 | A3i | 750-952 |
| SERINE/THREONINE-PROTEIN KINASE PLK (EC 2.7.1.-) (PLK-1) (STPK13) | U01038 | A3j | 1259-1502 |
| PHOSPHOLIPASE D1 | U38545 | A3k | 1330-3233 |
| NEDD5 PROTEIN HOMOLOG. | D63878 | A3l | 2862-3961 |
| CDC10 PROTEIN HOMOLOG | S72008 | A3m | 381-675 |
| CDC27HS PROTEIN | U00001 | A3n | 66-379 |
| UBIQUITIN-CONJUGATING ENZYME E2-CDC34 | L22005 | A4a | 870-3474 |
| CDC16HS. | U18291 | A4b | 249-550 |
| CDC37 HOMOLOG. | U63131 | A4c | 45-378 |
| CDC6-RELATED PROTEIN | U77949 | A4d | 519-1464 |
| EXTRACELLULAR SIGNAL-REGULATED KINASE 1 (EC 2.7.1.-) (ERK1) (INSULIN- STIMULATED MAP2 KINASE) (MAP KINASE 1) (MAPK 1) (P44 ERK1) (ERT2) (P44-MAPK) (MICROTUBULE-ASSOCIATED PROTEIN-2 KINASE). | X60188 | A4e | 216-447 |
| EXTRACELLULAR SIGNAL-REGULATED KINASE 3 (EC 2.7.1.-) (ERK3) (MAP KINASE ISOFORM P97) (P97-MAPK). | X80892 | A4f | 754-1094 |
| EXTRACELLULAR SIGNAL-REGULATED KINASE 4 (EC 2.7.1.-) (ERK4) (MAP KINASE ISOFORM P63) (P63-MAPK). | X59727 | A4g | 806-1267 |
| EXTRACELLULAR SIGNAL-REGULATED KINASE 5 (EC 2.7.1.-) (ERK5) (ERK4) (BMK1 KINASE) | U25278 | A4h | 2678-2994 |
| EXTRACELLULAR SIGNAL-REGULATED KINASE 6 (EC 2.7.1.-) (ERK6) (ERK5) | X79483 | A4i | 1010-1267 |
| | | A4j | 530-831 |

TABLE 3 (CONT)

| Cell Cycle/Growth Regulators | GenBank # | Array Coordinate | Position |
|--|------------------|------------------|-----------|
| MITOGEN-ACTIVATED PROTEIN KINASE P38 (EC 2.7.1.-) (MAP KINASE P38) (CYTOKINE SUPPRESSIVE ANTI-INFLAMMATORY DRUG BINDING PROTEIN) (CSAID BINDING PROTEIN) (CSBP) (MAX-INTERACTING PROTEIN 2) (MAP KINASE MXI2). | L35253; [L35263] | | |
| STRESS-ACTIVATED PROTEIN KINASE JNK1 (EC 2.7.1.-) (C-JUN N-TERMINAL KINASE 1) (JNK-46) | L26318 | A4k | 925-1204 |
| STRESS-ACTIVATED PROTEIN KINASE JNK2 (EC 2.7.1.-) (C-JUN N-TERMINAL KINASE 2) (JNK-55). | L31951 | A4l | 952-1263 |
| STRESS-ACTIVATED PROTEIN KINASE JNK3 (EC 2.7.1.-) (C-JUN N-TERMINAL KINASE 3) (JNK3) (MAP KINASE P49 3F12). | U34819; [U07620] | A4m | 638-1000 |
| DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 5 (EC 2.7.1.-) (MAP KINASE KINASE 5) (MAPKK 5) (MAP/ERK KINASE 5). | U25265 | A4n | 1018-1413 |
| DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 6 (EC 2.7.1.-) (MAP KINASE KINASE 6) (MAPKK 6) (MAP/ERK KINASE 6) (SAPKK3) | L05624 | A5a | 629-847 |
| MEK KINASE 3 | U78876 | A5c | 1060-1389 |
| PCNA (CYCLIN) | M15796; [J04718] | A5d | 1195-1453 |
| PIN1 | U49070 | A5e | 157-436 |
| RBP1 (RETINOBLASTOMA-BINDING PROTEIN) | S57153; S57160 | A5f | 624-1075 |
| E2F-1 pRB-binding protein | M96577 | A5g | 2676-2889 |
| E2F-3 | Y10479 | A5h | 899-1595 |
| E2F-5 | U15642 | A5i | 698-897 |
| E2F-related transcription factor (DP-1) | L23959 | A5j | 645-922 |
| DP2 (Humdp2), dimerization partner of E2F | U18422 | A5k | 935-1186 |
| RBQ-3 | X85134 | A5l | 1603-1838 |
| GROWTH-ARREST-SPECIFIC PROTEIN 1 (GAS-1). | L13698 | A5m | 359-603 |
| growth inhibitor p33ING1 (ING1) | AF001954 | A5n | 1550-1701 |
| Abl interactor 2 (Abl-2) + Abl binding protein 3 (AblBP3) [ArgBP1B] | U23435; U31089 | A6a | 722-983 |
| GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2 ADAPTOR PROTEIN) (ASH PROTEIN). | L29511; [M96995] | A6b | 1049-1203 |
| GRB-IR / GRB10 | U69276 | A6c | 355-573 |
| RAF ONCOGENE | X03484 | A6d | 358-1155 |
| raf.b. | M95712 | A6e | 1704-1989 |
| Jun B TRANSACTIVATOR | M29039 | A6f | 866-1144 |
| N-myc | M13228 | A6g | 1197-1442 |
| | | A6h | 761-1188 |

TABLE 3 (CONT)

| Cell Cycle/Growth Regulators | GenBank # | Array Coordinate | Position |
|---|--|------------------|-----------|
| C-myc binding protein | D89667 | A6i | 218-490 |
| INTERMEDIATE FILAMENT MARKERS | | | |
| KERATIN, TYPE I CYTOSKELETAL 9 (CYTOKERATIN 9) (K9) (CK 9). | Z29074; [S69510] | A6j | 652-1781 |
| KERATIN, TYPE I CYTOSKELETAL 10 (CYTOKERATIN 10) (K10) (CK 10) | M19156 | A6k | 295-497 |
| KERATIN, TYPE I CYTOSKELETAL 12 (CYTOKERATIN 12) (K12) | D78367 | A6l | 455-624 |
| KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK 13) + KERATIN, TYPE I CYTOSKELETAL 15 (CYTOKERATIN 15) (K15) (CK 15) + KERATIN, TYPE I CYTOSKELETAL 17 (CYTOKERATIN 17) (K17) (CK 17) (39.1) | X52426; X07696; X62571 | | |
| KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) | J00124 | A6m | 383-1001 |
| KERATIN, TYPE I CYTOSKELETAL 16 (CYTOKERATIN 16) (K16) (CK 16); pseudo-keratin K16 type I | M21772; M20336 | A6n | 339-839 |
| KERATIN, TYPE I CYTOSKELETAL 18 (CYTOKERATIN 18) (K18) (CK 18) | M26326 | A7a | 32-522 |
| KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19) | Y00503 | A7b | 706-971 |
| KERATIN, TYPE II CYTOSKELETAL 1 (CYTOKERATIN 1) (K1) (CK 1) (67 KD CYTOKERATIN) (HAIR ALPHA PROTEIN) | M98776 | A7c | 726-1124 |
| KERATIN, TYPE II CYTOSKELETAL 2 ORAL (CYTOKERATIN 2P) (K2P) (CK 2P) | M99063 | A7d | 894-1459 |
| KERATIN, TYPE II CYTOSKELETAL 2 EPIDERMAL (CYTOKERATIN 2E) (K2E) (CK 2E) | M99061 [S43646] | A7e | 2167-2455 |
| KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4) | X67663 | A7f | 1091-1450 |
| KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5) (58 KD CYTOKERATIN) | M21389 | A7g | 66-404 |
| KERATIN, TYPE II CYTOSKELETAL 6 (CYTOKERATIN 6A) (CK 6A) (K6A KERATIN) + (CYTOKERATIN 6B) (CK 6B) (K6B KERATIN) + (CYTOKERATIN 6C) (CK 6C) (K6C KERATIN) + (CYTOKERATIN 6D) (CK 6D) (K6D KERATIN) + (CYTOKERATIN 6E) (CK 6E) (K6E KERATIN) + (CYTOKERATIN 6F) | J00269; V01516; L42592; L00205; L42601; L42610; L42611; L42612 | A7h | 93-682 |
| KERATIN, TYPE II CYTOSKELETAL 6B (CYTOKERATIN 6B) (CK 6B) (K6B KERATIN) | L42592; L00205 | A7i | 689-880 |
| KERATIN, TYPE II CYTOSKELETAL 7 (CYTOKERATIN 7) (K7) (CK 7) | X03212 | A7j | 275-414 |
| KERATIN, TYPE II CYTOSKELETAL 8 (CYTOKERATIN 8) (K8) (CK 8) | M34225 | A7k | 1154-1430 |
| VIMENTIN | X56134 [M14144] | A7m | 1190-1474 |
| DESMIN | U59167 | A7n | 460-740 |
| | | | 1063-1364 |

TABLE 3 (CONT)

| Cell Cycle/Growth Regulators | GenBank # | Array Coordinate | Position |
|--|----------------------------------|------------------|-----------|
| QUADRANT B | | | |
| APOPTOSIS | | | |
| BCL2 | M14745 | B1a | 5078-5382 |
| Bcl2 and p53 binding protein Bbp/53BP2 (BBP/53BP2) | U58334 | B1b | 3129-3376 |
| BAX | L22474 | B1c | 227-478 |
| APOPTOSIS REGULATOR BCL-W | U59747 | B1d | 121-403 |
| INDUCED MYELOID LEUKEMIA CELL DIFFERENTIATION PROTEIN | L08246 | | |
| MCL-1 (ORF is at nt. 61-1053; ML) | | B1e | 697-977 |
| BCL2-RELATED PROTEIN A1 (BFL-1 PROTEIN) (HEMOPOIETIC-SPECIFIC EARLY RESPONSE PROTEIN) (GRS PROTEIN) | U29680 | B1f | 64-293 |
| BCL-2 INTERACTING KILLER (APOPTOSIS INDUCER NBK) (BP4) (BIP1) (BIK) | X89986; [U34584] | B1g | 935-1200 |
| BCL-2 HOMOLOGOUS ANTAGONIST/KILLER (APOPTOSIS REGULATOR BAK) | U23765; [U16812; U16811; X84213] | B1h | 1371-1661 |
| BAD PROTEIN (BCL-2 BINDING COMPONENT 6). | U66879 | B1i | 408-749 |
| BCL-2 BINDING ATHANOGENE-1 (BAG-1) (GLUCOCORTICOID RECEPTOR-ASSOCIATED PROTEIN RAP46). | S83171; [Z35491] | B1j | 511-830 |
| serine/threonine protein kinase, NIK; binds specifically to TRAF2 Casper, a FADD- and caspase-related inducer of apoptosis [CASH-alpha+ CASH-beta] (FLAME-1) (FLICE-like inhibitory protein) | Y10256 | B1k | 3776-4036 |
| death domain containing protein CRADD, apoptotic adaptor molecule for caspase-2 and FasL/TNF receptor-interacting protein RIP | AF010127[Y14039; Y14040] | B1l | 363-787 |
| TNF receptor-1 associated protein (TRADD) | U84388 | | |
| cell death protein kinase RIP | L41690 | B1m | 369-604 |
| DAXX, a FAS-binding protein that activates JNK and apoptosis | U25994; [U50062] | B1n | 1009-1313 |
| Apo-2 ligand (TNF-related apoptosis inducing ligand TRAIL) | AF015956 | B2a | 848-1123 |
| TRAF-INTERACTING PROTEIN 1-TRAF (TRAF family member-associated NF-kB activator TANK) | U57059 | B2b | 804-1030 |
| | U59863; [U63830] | B2c | 211-616 |
| TRAF5 | | B2d | 674-887 |
| TRAF6 | U69108 | B2e | 1318-1694 |
| TRAF-interacting protein (TRIP) | U78798; [L81153] | B2f | 1689-1961 |
| tumor necrosis factor type 2 receptor associated protein (TRAP3) | U77845 | B2g | 154-387 |
| CD40 RECEPTOR ASSOCIATED FACTOR 1 (CRAFT1) (CAP-1), (LMP1 associated protein) | U12597 | B2h | 1207-1566 |
| INHIBITOR OF APOPTOSIS PROTEIN 1 (HIAP1) (HIAP-1) (C-IAP2) (TNFR2-TRAF SIGNALING COMPLEX PROTEIN 1) (IAP HOMOLOG C) (IAP1) (MIHC). | U21092; [U15637; L38509; U19260] | B2i | 980-1322 |
| | U45878; [U37546] | | |
| | | B2j | 1444-1848 |

TABLE 3 (CONT)

| Cell Cycle/Growth Regulators | GenBank # | Array Coordinate | Position |
|--|---|------------------|-----------|
| INHIBITOR OF APOPTOSIS PROTEIN 2 (HIAP2) (HIAP-2) (C-IAP1) (TNFR2- TRAF SIGNALING COMPLEX PROTEIN 2) (IAP HOMOLOG B) (IAP2) (MIHB). | U45879; [U37547] | | |
| X-LINKED INHIBITOR OF APOPTOSIS PROTEIN (X-LINKED IAP) (IAP-LIKE PROTEIN) (HILP). | U45880; [U32974] | B2k | 266-621 |
| p53-dependent cell growth regulator CGR19 | U66469 | B2l | 2000-2363 |
| cytotoxic ligand TRAIL receptor | U90875 | B2m | 28-301 |
| (ICE) (INTERLEUKIN-1 BETA CONVERTING ENZYME) (P45) (CASPASE-1) | U13699; [M87507; X65019] | B2n | 290-548 |
| (CASPASE-2) (ICH-1L) (ICH-1S) | U13021; [U13022] | B3a | 5078-5282 |
| APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CASPASE-3) (CPP32) (YAMA PROTEIN) (CASPASE-3) isoform alpha | U13737 | B3b | 851-1218 |
| ICH-2 PROTEASE PRECURSOR (EC 3.4.22.-) (TX PROTEASE) (ICEREL-II) (CASPASE-4) + CASPASE-5 PRECURSOR (EC 3.4.22.-) (ICH-3 PROTEASE) (TY PROTEASE (ICEREL-III). | U28014; U28015 | B3c | 2007-2434 |
| CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) isoform beta + isoform alpha | U20537; U20536 | B3d | 763-11-07 |
| CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) (Lic2) | U37448 | B3e | 387-697 |
| CASPASE-8 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 5) (MORT1-ASSOCIATED CED-3 HOMOLOG) (MACH) (FADD-HOMOLOGOUS ICE/CED-3-LIKE PROTEASE) (FADD-LIKE ICE) (FLICE) (APOPTOTIC CYSTEINE PROTEASE) (APOPTOTIC PROTEASE MCH-5) (CAP4) (CASP8) (MCH5) isoform alpha | U60520; U58143; X98172; X98173; X98174; AF00962 | B3f | 1042-1413 |
| CASPASE-8 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 5) (MORT1-ASSOCIATED CED-3 HOMOLOG) (MACH) (FADD-HOMOLOGOUS ICE/CED-3-LIKE PROTEASE) (FADD-LIKE ICE) (FLICE) (APOPTOTIC CYSTEINE PROTEASE) (APOPTOTIC PROTEASE MCH-5) (CAP4) (CASP8) (MCH5) isoform beta | U60520; U58143; X98172; X98173; X98174; AF00962; X98176; X98175; X98177; X98178 | B3g | 1327-1607 |
| CASPASE-9 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 6) (ICE-LAP6) (APOPTOTIC PROTEASE MCH-6) | U56390; [U60521] | B3h | 475-954 |
| ICE-LIKE APOPTOTIC PROTEASE 4 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-4) (CASPASE-10) | U60519 | B3i | 986-1289 |
| DEATH-ASSOCIATED PROTEIN 3 (DAP-3) (ionizing radiation resistance conferring protein) | U18321; [X83544] | B3j | 2276-2690 |
| DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1). | X76104 | B3k | 856-1114 |
| | | B3l | 1988-2321 |

TABLE 3 (CONT)

| Cell Cycle/Growth Regulators | GenBank # | Array Coordinate | Position |
|--|----------------------------------|------------------|-----------|
| Fas-activated serine/threonine kinase (FAST) phosphorylates TIA-1 | X85779 | B3m | 865-1239 |
| PDCD2 | S78085 | B3n | 406-694 |
| FAS/APO 1 | Z70519 | B4a | 1493-1887 |
| FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL) (APT1LG1) (FASL) | D38122; [U08137] | B4b | 1400-1782 |
| WSL-LR, WSL-S1, WSL-S2 + TRAMP (Apo-3) (DDR3) | Y09392; [U75380; U74611; U83597] | B4c | 1407-1671 |
| AK1 (rac protein kinase alpha, protein kinase B, c-Akt) | M63167 | B4d | |
| AKT2 (rac protein kinase beta) | M77198; [M95936] | B4e | 1867-2099 |
| TNF-alpha converting enzyme | U69611 | B4f | 1540-1746 |
| death receptor 5 (DR5) | AF016268 | B4g | 273-552 |
| BRAG-1=brain-related apoptosis gene/Bcl-2 homolog | S82185 | B4h | 351-985 |
| seven in absenlia homolog | U63295 | B4i | 239-523 |
| RATS1 | U37688 | B4j | 1247-1367 |
| DNA fragmentation factor-45 | U91985 | B4k | 485-1592 |
| secreted apoptosis related protein 1 | AF017986 | B4l | 189-974 |
| secreted apoptosis related protein 3 (SARP3) | AF017988 | B4m | 702-841 |
| apoptosis-related protein TFAR15 (TFAR15) | AF022385 | B4n | 365-520 |
| calmodulin dependent phosphodiesterase PDE1B1 | U56976 | B5a | 414-549 |
| glutathione-S-transferase homolog | U90313 | B5b | 97-837 |
| CD27BP (Siva) | U82938 | B5c | 406-625 |
| chromosome segregation gene homolog CAS | U33286 | B5d | 674-1247 |
| apoptosis inhibitor survivin | U75285 | B5e | 386-720 |
| p53 induced protein | AF010310 AF010311 | B5f | 29-771 |
| Pig3 (PIG3) | AF010309 | B5g | 398-1223 |
| Pig7 (PIG7) | AF010312 | B5h | 173-322 |
| Pig10 (PIG10) | AF010314 | B5i | 437-1623 |
| Pig11 (PIG11) | AF010315 | B5j | 748-1304 |
| Pig12 (PIG12) | AF010316 | B5k | 97-531 |
| GTP-binding protein (rhoA) | L25080 | B5l | 290-572 |
| cdc42 homolog (G25K) [brain isoform + placental isoform] | M35543; [M57298] | B5m | 321-468 |
| ONCOGENES/TUMOR SUPPRESSORS | | | |
| C-FMS PROTO ONCOGENE | X03663 | B5n | 2568-2880 |
| C-fos | K00650 | B6a | 2949-3181 |
| C-kit | X06182 | B6b | 1981-2375 |
| PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC (EC 2.7.1.112) (P60-SRC) (C-SRC). | HT2291; [K03214; X03996] | B6c | 893-1189 |
| PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FGR (EC 2.7.1.112) (P55-FGR) (C-FGR). | M19722 | B6d | 521-856 |

TABLE 3 (CONT)

| Cell Cycle/Growth Regulators | GenBank # | Array Coordinate | Position |
|---|------------------|------------------|-------------|
| DNA MISMATCH REPAIR PROTEIN MSH2 | U04045; [L47583] | B6e | 1496-2178 |
| DNA MISMATCH REPAIR PROTEIN MSH6 (mutS - ALPHA 160 KD SUBUNIT) (GT MISMATCH BINDING PROTEIN) (GTBP) (GTMBP) (P160) | U54777 | | |
| K-RAS; ONCOGENE | M54968 | B6f | 591-1100 |
| MET | J02958 | B6g | 352-604 |
| p53 | M14694; [M14695] | B6h | 932-1242 |
| BREAST CANCER TYPE 2 SUSCEPTIBILITY PROTEIN | U43746 | B6i | 690-964 |
| BRCA1-ASSOCIATED RING DOMAIN PROTEIN | U76638 | B6j | 10056-10346 |
| MDM2 PROTEIN (P53-ASSOCIATED PROTEIN) + MDM2-A (GB: U33199) + MDM2-C (GB: U33201) | Z12020; [M92424] | B6k | 1493-1801 |
| MDM2-like p53-binding protein (MDMX) | AF007111 | B6l | 920-1232 |
| p73, a monoallelically expressed p53-related protein | Y11416 | B6m | 405-681 |
| RB2/p130 | X74594 | B6n | 627-993 |
| RBA/p48 | X74262 | B7a | 951-1213 |
| RBp2 retinoblastoma binding protein | S68431 | B7b | 605-974 |
| RBQ1 retinoblastoma binding protein | X85133 | B7c | 2339-2642 |
| PROTO-ONCOGENE TYROSINE-PROTEIN KINASE RECEPTOR RET PRECURSOR (EC 2.7.1.112) (C-RET), [Papillary thyroid carcinoma-encoded protein] | M31213; [M57464] | B7d | 1701-1930 |
| Retinoblastoma susceptibility (RB1 retinoblastoma-assoc) | M15400 | B7e | 2285-2631 |
| SKY (DTK) (TYRO3) (RSE) | D17517 | B7f | 2839-3101 |
| YES | M15990 | B7g | 2132-2597 |
| TYROSINE-PROTEIN KINASE BTK (EC 2.7.1.112) (BRUTON'S TYROSINE KINASE)(AGAMMAGLOBULINAEMIA TYROSINE KINASE) (ATK) (B CELL PROGENITOR KINASE) (BPK) (BTK) (AGMX1) | U10087 X58957 | B7h | 1325-1676 |
| TYROSINE-PROTEIN KINASE ABL2 (EC 2.7.1.112) (TYROSINE KINASE ARG) (ABL) | M35296 | | |
| TYROSINE-PROTEIN KINASE ZAP-70 (EC 2.7.1.112) (70 KD ZETA-ASSOCIATED PROTEIN) (ZAP70) | L05148 | B7i | 380-1430 |
| SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA (TRANSCRIPTION FACTOR ISGF-3 COMPONENTS P91/P84) (STAT1) | M97935 | B7j | 493-1656 |
| SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 2 (P113) (STAT2) | U18671 M97934 | B7k | 1-584 |
| SIGNAL TRANSDUCER AND TRANSCRIPTION ACTIVATOR 5B (STAT5B) | U47686 | B7l | 638-1376 |
| | | B7m | 1105-1480 |
| | | B7n | 831-1135 |
| QUADRANT C | | | |

TABLE 3 (CONT)

| Cell Cycle/Growth Regulators | GenBank # | Array Coordinate | Position |
|--|------------------|------------------|-----------|
| DNA DAMAGE RESPONSE/REPAIR/RECOMBINATION | | | |
| DNA-DEPENDENT PROTEIN KINASE (DNA-PK) + DNA DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT (DNA-PKcs) (XRCC7) | U35835; [U47077] | | |
| | | C1a | 2250-2680 |
| | U33841 | C1b | 8938-9135 |
| ATAXIA TELANGIECTASIA (ATM) | L34075 | C1c | 6750-7088 |
| FKBP-RAPAMYNSIN ASSOCIATED PROTEIN (FRAP) | | | |
| ATP-DEPENDENT DNA HELICASE II, 70 KD SUBUNIT (LUPUS KU AUTOANTIGEN PROTEIN P70) (70 KD SUBUNIT OF KU ANTIGEN) (THYROID-LUPUS AUTO-ANTIGEN) (TLAA) (KU70) (CTC BOX BINDING FACTOR 75 KD SUBUNIT) (CTCBF) (CTC75) (XRCC6) | M32865; [S38729] | | |
| ATP-DEPENDENT DNA HELICASE II, 86 KD SUBUNIT (LUPUS KU AUTOANTIGEN PROTEIN P86) (86 KD SUBUNIT OF KU ANTIGEN) (THYROID-LUPUS AUTOANTIGEN) (TLAA) (CTC BOX BINDING FACTOR 85 KD SUBUNIT) (CTCBF) (CTC85) (NUCLEAR FACTOR IV) (KU80) (XRCC5) | M30938 | C1d | 1729-1974 |
| DNA EXCISION REPAIR PROTEIN ERCC1 | M13194 | C1e | 2340-2784 |
| DNA LIGASE III (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP)) (DNL3) | X84740 | C1f | 625-938 |
| DNA LIGASE IV (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP)) (DNL4) | X83441 | C1g | 2460-2780 |
| DNA POLYMERASE ALPHA | X06745 | C1h | 2787-3074 |
| DNA REPAIR PROTEIN RAD50 | U63139 | C1i | 3721-4093 |
| DNA REPAIR PROTEIN RAD51 HOMOLOG [Replication protein A (E coli RecA homolog, RAD51 homolog)] | D13804 | C1j | 5117-5435 |
| DNA REPAIR PROTEIN RAD52 HOMOLOG | U12134 | C1k | 867-1159 |
| DNA TOPOISOMERASE I | J03250 | C1l | 1528-1733 |
| DNA TOPOISOMERASE II ALPHA ISOZYME | J04088 | C1m | 2388-2796 |
| DNA-REPAIR PROTEIN COMPLEMENTING XP-B CELLS (XERODERMA PIGMENTOSUM GROUP B COMPLEMENTING PROTEIN) (DNA EXCISION REPAIR PROTEIN ERCC3) (BASAL TRANSCRIPTION FACTOR 2 89 KD SUBUNIT) (BTF2-p89) (TFIIH 89 KD SUBUNIT) | M31899 | C1n | 2459-2883 |
| DNA-REPAIR PROTEIN COMPLEMENTING XP-D CELLS (XERODERMA PIGMENTOSUM GROUP D COMPLEMENTING PROTEIN) (DNA EXCISION REPAIR PROTEIN ERCC-2) | X52221; [HT1175] | C2a | 2109-2466 |
| DNA-REPAIR PROTEIN XRCC1 | | | |
| DNA-REPAIR PROTEIN COMPLEMENTING XP-G CELLS (XERODERMA PIGMENTOSUM GROUP G COMPLEMENTING PROTEIN) (DNA EXCISION REPAIR PROTEIN ERCC-5) | M36089 | C2b | 1520-1821 |
| | L20046; [X69978] | C2c | 1226-1539 |
| | | C2d | 1374-1638 |

TABLE 3 (CONT)

| Cell Cycle/Growth Regulators | GenBank # | Array Coordinate | Position |
|--|---------------------------|------------------|-----------|
| GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD153 (DNA-DAMAGE INDUCIBLE PROTEIN) (CHOP) | S40706 [S62138] | C2e | 480-789 |
| GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD45 (DNA-DAMAGE INDUCIBLE TRANSCRIPT 1) (DDIT1) | M60974 | C2f | 526-886 |
| METHYLATED-DNA--PROTEIN-CYSTEINE METHYLTRANSFERASE (6-O-METHYLGUANINE-DNA METHYLTRANSFERASE) (MGMT) | M29971 | C2g | 241-546 |
| MUSCLE-SPECIFIC DNASE I-LIKE [DNase X] (XIB) | X90392 ; [L40817; U06846] | C2h | 2038-2427 |
| DNA MISMATCH REPAIR PROTEIN MLH1 (mutL HOMOLOG) | U07418 | C2i | 1765-2020 |
| RAD | L24564 | C2j | 469-780 |
| ACTIVATOR 1 36 KD SUBUNIT (REPLICATION FACTOR C 36 KD SUBUNIT) (RFC36) | L07540 | C2k | 708-1051 |
| ACTIVATOR 1 37 KD SUBUNIT (REPLICATION FACTOR C 37 KD SUBUNIT) (RFC37) | M87339 | C2l | 98-355 |
| ACTIVATOR 1 38 KD SUBUNIT (REPLICATION FACTOR C 38 KD SUBUNIT) (RFC38) | L07541 | C2m | 438-762 |
| ACTIVATOR 1 40 KD SUBUNIT (REPLICATION FACTOR C 40 KD SUBUNIT) (RFC40) | M87338 | C2n | 882-1286 |
| REPLICATION PROTEIN A 70 KD DNA-BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE STRANDED DNA-BINDING PROTEIN) | M63488 | C3a | 1498-1838 |
| SUPEROXIDE DISMUTASE [Superoxide dismutase 1 (Cu/Zn)] | HT3218 [K00065] | C3b | 198-496 |
| TRANSCRIPTIONAL ACTIVATOR PROTEIN PUR-ALPHA | M96684 | C3c | 563-855 |
| HHR6A (YEAST RAD6 HOMOLOG) (UBIQUITIN-CONJUGATING ENZYME) (UBCA) | M74524 | C3d | 175-433 |
| UV EXCISION REPAIR PROTEIN RAD23 [xeroderma pigmentosum group C repair complementing protein HHR23A] | D21235 | C3e | 355-632 |
| CELL FATE/DEVELOPMENT REGULATORS | | | |
| -Notch pathway | | | |
| Notch1 | M73980 | C3f | 2701-2965 |
| Notch2 | U77493 | C3g | 373-658 |
| notch group protein (N) | M99437 | C3h | 647-1210 |
| Notch4 | U95299 | C3i | 3014-3169 |
| Jagged 1 | AF028593 | C3j | 3884-4117 |
| Jagged 2 | AF003521 | C3k | 1027-1241 |
| DELTA-LIKE PROTEIN PRECURSOR (CONTAINS: FETAL ANTIGEN 1) (FA1) (DLK) + ADRENAL SPECIFIC 30kd PROTEIN GB: X17544 | U15979; [Z12172] | | |
| manic fringe | U94352 | C3l | 1050-1403 |
| | | C3m | 979-1235 |

TABLE 3 (CONT)

| Cell Cycle/Growth Regulators | GenBank # | Array Coordinate | Position |
|---|--------------------------|------------------|-----------|
| lunatic fringe | U94354 | C3n | 563-857 |
| -Wnt pathway | | | |
| WNT2 OR IRP | X07876 | C4a | 899-1252 |
| Wnt-5a | L20861 | C4b | 1036-1281 |
| WNT-8B | X91940 | C4c | 164-447 |
| WNT-10B | X97057 | C4d | 330-635 |
| Wnt-13 | Z71621 | C4e | 569-847 |
| frizzled | L37882 | C4f | 1491-1756 |
| frizzled-related FrzB (Fritz) (frizzled (fr)) | U24163; [U91903; U68057] | | |
| frizzled 5 | U43318 | C4g | 590-819 |
| frizzled homolog (FZD3) | U82169 | C4h | 936-1091 |
| dishevelled (DVL) + dishevelled 3 (DVL3) | U49262; [U75651] | C4i | 865-1182 |
| dishevelled homolog (DVL) | U46461 | C4j | 1311-1610 |
| -Hedgehog pathway | | C4k | 1409-1586 |
| sonic hedgehog (SHH) | L38518 | C4l | 164-474 |
| patched homolog (PTC) | U43148 | C4m | 3179-4050 |
| smoothed | U84401 | C4n | 503-789 |
| RECEPTORS | | | |
| 5T4 ONCOFETAL ANTIGEN | Z29083 | C5a | 748-981 |
| AXL (TYROSINE-PROTEIN KINASE RECEPTOR UFO) | M76125 | C5b | 2045-2348 |
| CATION-INDEPENDENT MANNANOSE-6-PHOSPHATE RECEPTOR | Y00285; [J03528] | | |
| [insulin-like growth factor receptor II, IGFR-2] | | C5c | 1394-1831 |
| CDW40; NERVE GROWTH FACTOR RECEPTOR-RELATED B- | X60592 | | |
| LYMPHOCYTE ACTIVATION MOLECULE | | C5d | 198-605 |
| EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR (EC | K03193; [X00588; X00663; | | |
| 2.7.1.112). (EGFR) (ERBB1) | U48722] | C5e | 3410-3757 |
| EPS 15 (AF-1P PROTEIN) | U07707; [Z29064] | C5f | 1828-2140 |
| EPS8 | U12535 | C5g | 2293-2645 |
| ERBB4 | L07868 | C5h | 3570-3965 |
| ERYTHROPROTEIN RECEPTOR | M60459 | C5i | 1423-1740 |
| FAU | X65923 | C5j | 8-344 |
| GARP | Z24680 | C5k | 3399-3777 |
| HER2 (ERB-B2) | M11730; [M95667] | C5l | 2556-2722 |
| HER3 (ERB-B3) | M28366; [M34309] | C5m | 3886-4139 |
| HGF ACTIVATOR | D14012 | C5n | 1487-1845 |
| HGF ACTIVATOR LIKE | D49742; [S83182] | C6a | 311-595 |
| IGFBP COMPLEX ACID LABILE CHAIN | D25216 | C6b | 1509-2669 |
| IGFBP2 | M35410 | C6c | 680-1071 |

TABLE 3 (CONT)

| Cell Cycle/Growth Regulators | GenBank # | Array Coordinate | Position |
|---|--|------------------|-----------|
| IGFBP3 (GROWTH HORMONE-DEPENDENT INSULIN-LIKE GROWTH FACTOR-BINDING PROTEIN) | M31159; [M35878] | C6d | 451-744 |
| IGFBP4 | M62403 | C6e | 657-967 |
| IGFBP5 | M65062 | C6f | 356-602 |
| IGFBP6 | M62402 | C6g | 345-536 |
| INSULIN-LIKE GROWTH FACTOR I RECEPTOR | X04434 | C6h | 3413-3904 |
| BASIC FIBROBLAST GROWTH FACTOR RECEPTOR 1 PRECURSOR (BFGF-R) (EC 2.7.1.112) (FMS-LIKE TYROSINE KINASE-2) (C-FGR) (FGFR1) (FLG) (FGFR) (FLT2). (HBGF-R-ALPHA-A1) (HBGF-R-ALPHA-A2) (HBGF-R-ALPHA-A3) + FGFR SECRETED FORM (M34188) | M37722; [X66945; M63887; M63888; M63889; M34186; M34641] | | |
| NERVE GROWTH FACTOR RECEPTOR | M14764 | C6i | 1746-1967 |
| PDGFR-ALPHA | M21574 | C6j | 2762-3242 |
| PDGFR-BETA | M21616 | C6k | 5118-5583 |
| transmembrane receptor precursor (PTK7); COLON CARCINOMA KINASE-4 (CKK4) | U33635; [U40271] | C6l | 842-1133 |
| SEX GENE | X87852 | C6m | 3507-3784 |
| TRANSFORMING GROWTH FACTOR-BETA TYPE III RECEPTOR | L07594 | C6n | 209-433 |
| TRANSMEMBRANE PROTEIN TMP21 | X97442 | C7a | 3358-3592 |
| HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRK1 TRANSFORMING TYROSINE KINASE PROTEIN) (P140-TRKA) + trk-T3 (P68 TRK-T3 ONCOPROTEIN) | X03541 | C7b | 380-1176 |
| trk-T3 (P68 TRK-T3 ONCOPROTEIN) | X85960 | C7c | 1816-2118 |
| trk-B | U12140 | C7d | 252-1112 |
| trk-C | U05012 | C7e | 1006-1384 |
| TUMOR NECROSIS FACTOR RECEPTOR 1 | M33294 | C7f | 359-765 |
| TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 2) (TBPI) (P80) (TNF-R2) (P75) (CD120B) (TNFR2) (TNFR) | M32315; [M55994] | C7g | 1570-1817 |
| RETINOIC ACID RECEPTOR ALPHA1 (RAR- ALPHA1) + PML-RAR protein | M73779; [X06538; [X06614] | C7h | 3359-3543 |
| retinoic acid receptor alpha [RETINOIC ACID RECEPTOR RXR-ALPHA (RXRA)] | X52773 | C7i | 2935-3238 |
| retinoic acid receptor epsilon [RETINOIC ACID RECEPTOR BETA-2 (RAR BETA-2) (RAR-EPSILON)] | X07282; [Y00291] | C7j | 352-616 |
| retinoic acid receptor gamma [RETINOIC ACID RECEPTOR GAMMA] | M24857; [M38256; M57707; M32074] | C7k | 1315-1633 |
| retinoic acid receptor rxr-beta [RETINOIC ACID RECEPTOR RXR-BETA] | M84820; [X63522] | C7l | 1569-1834 |
| | | C7m | 643-1135 |

TABLE 3 (CONT)

| Cell Cycle/Growth Regulators | GenBank # | Array Coordinate | Position |
|--|----------------------------------|------------------|-----------|
| THROMBOPOIETIN RECEPTOR | U68182 | C7n | 5117-5435 |
| QUADRANT D | | | |
| CELL ADHESION, MOTILITY, AND INVASION | | | |
| CARTILAGE-SPECIFIC PROTEOGLYCAN CORE PROTEIN (CSPCP) | M55172 | | |
| (AGGRECAN 1)(CHONDROITIN SULFATE PROTEOGLYCAN CORE | | | |
| PROTEIN 1) | | | |
| byglycan | J04599 | D1a | 6705-6956 |
| CD34 | M81104 | D1b | 854-1129 |
| CD59 | M34871 | D1c | 598-960 |
| CHONDROITIN/DERMATAN SULFATE PROTEOGLYCAN CORE | M14219 | D1d | 105-1163 |
| PROTEIN (DECORIN) (PG-S2) (PG40) | | | |
| COLLAGEN (-6000BP) | D21337 | D1e | 712-896 |
| collagen type I | X55525 | D1f | 5342-5588 |
| collagen type II alpha-1 | X16468 | D1g | 428-741 |
| collagen type III pro-alpha-1 | X14420 | D1h | 3604-3751 |
| collagen type IV alpha | X05610 | D1i | 3867-4046 |
| collagen type IV alpha-3 | M92993 | D1j | 882-1113 |
| collagen type VI alpha-1 | X15879 | D1k | 2296-2545 |
| collagen type VI alpha-2 | M34570 | D1l | 316-688 |
| collagen type VI alpha-3 | X52022 | D1m | 203-396 |
| collagen type VII alpha-1 | X57527 | D1n | 640-1487 |
| collagen type XI alpha-1 | J04177 | D2a | 612-1772 |
| collagen type XI pro-alpha-2 | U32169 | D2b | 2884-3091 |
| collagen type XVI alpha-1 | M92642 | D2c | 4473-4769 |
| collagen type XVIII alpha | L22548 | D2d | 4816-5991 |
| LAM3AH (LAMA4) | X70904; [X91171] | D2e | 2300-2539 |
| LAMB2 (LAMININ) | S77512 | D2f | 1018-1388 |
| laminin B1 | M61916 | D2g | 3871-4158 |
| laminin B2 | J03202 | D2h | 3177-3554 |
| laminin, 37KD RECEPTOR | U43901 | D2i | 2878-3232 |
| netrin-2 | U86759 | D2j | 460-812 |
| nidogen | M30269 | D2k | 859-1147 |
| TENASCIN-C | X78565 | D2l | 2120-2428 |
| TENASCIN-R | X98085 | D2m | 6652-6924 |
| VERSICAN [isoforms , V1, V2, V3] | U16306; [X15998; U26555; D32039] | D2n | 3916-4165 |
| | | D3a | 189-974 |

TABLE 3 (CONT)

| Cell Cycle/Growth Regulators | GenBank # | Array Coordinate | Position |
|--|------------------|------------------|-----------|
| SPARC PRECURSOR (SECRETED PROTEIN ACIDIC AND RICH IN CYSTEINE) (OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40). | J03040 | | |
| THROMBOSPONDIN 1 PRECURSOR | X14787 | D3b | 280-642 |
| THROMBOSPONDIN 2 PRECURSOR | L12350 | D3c | 3187-3450 |
| VITRONECTIN PRECURSOR (SERUM SPREADING FACTOR) (S-PROTEIN) (CONTAINS: SOMATOMEDIN B) | X03168 | D3d | 3151-3531 |
| fibronectin | X02761 | D3e | 3721-4093 |
| RNA-binding protein Hel-N2; ELAV-like neuronal protein 1 | U12431; [U29943] | D3f | 6163-7290 |
| HEPARAN SULFATE PROTEOGLYCAN (HSPG2) | M85289 | D3g | 1006-1384 |
| integrin alpha | X68742 | D3h | 1232-1389 |
| integrin alpha2 [very late antigen-2 (vla-2)/collagen receptor alpha-2 subunit] | M28249; [X17033] | D3i | 2690-2976 |
| integrin alpha3 | M59911 | D3j | 2367-2664 |
| integrin alpha4 | L12002; [X16983] | D3k | 2564-2944 |
| integrin alpha5 [fibronectin receptor alpha subunit] | X06256 | D3l | 2709-3063 |
| integrin alpha6 | X53586; [X59512] | D3m | 2094-2367 |
| integrin alpha7B | X74295 | D3n | 3642-3988 |
| integrin alpha8 | L36531 | D4a | 255-591 |
| integrin alpha9 | D25303; [L24150] | D4b | 2709-3063 |
| integrin alphaE | L25851 | D4c | 708-980 |
| integrin beta1 | M34189 | D4d | 2279-2529 |
| integrin beta3 [PLATELET MEMBRANE GLYCOPROTEIN IIIA] | J02703; [M25108] | D4e | 701-1301 |
| integrin beta4 | X53587; [X52186] | D4f | 2038-2373 |
| integrin beta5 | J05633 | D4g | 5357-5697 |
| integrin beta6 | M35198 | D4h | 2278-2528 |
| integrin beta7 | M62880 | D4i | 1619-1901 |
| integrin beta8 | M73780 | D4j | 2562-2844 |
| Focal adhesion kinase | L13616 | D4k | 22-877 |
| Integrin-linked kinase (ILK) | U40282 | D4l | 2179-2631 |
| Protein tyrosine kinase Pyk2 (Cell adhesion kinase-beta, CAK-beta) (FAK2) | U43522; [L49207] | D4m | 1245-1530 |
| Paxillin | U14588 | D4n | 3658-3952 |
| Zyxin + Zyxin-2 | X94991; [X95735] | D5a | 1260-1644 |
| Zyxin related protein ZRP-1 | AF000974 | D5b | 585-1514 |
| beta 3-endonexin | U37139 | D5c | 1240-1466 |
| cytohesin-1; Sec7p-like protein | U59752 | D5d | 606-1504 |
| CD9 | M38690 | D5e | 43-338 |
| Ezrin (cytovillin 2) | X51521 | D5f | 372-962 |
| | | D5g | 1611-1883 |

TABLE 3 (CONT)

| Cell Cycle/Growth Regulators | GenBank # | Array Coordinate | Position |
|---|-----------------------------------|------------------|-----------|
| MERLIN (SCHWANNOMIN) (moesin-ezrin-radixin-like protein)(neurofibromatosis 2) | L11353; Z22664; X72657; L27133 | D5h | 355-674 |
| L1CAM | M74387 | D5i | 3197-3485 |
| N-CAM [NEURAL CELL ADHESION MOLECULE, PHOSPHATIDYLINOSITOL-LINKED ISOFORM; CD56] | X16841 | D5j | 2338-2646 |
| NINJURIN-1 | U72661 | D5k | 212-492 |
| opioid binding cell adhesion molecule | L34774 | D5l | 115-728 |
| DCC | X76132 | D5m | 893-1189 |
| P37NB | U32907 | D5n | 95-456 |
| PLEXIN | U52111 | D6a | 585-1514 |
| semaphorin (CD100) | U60800 | D6b | 2517-2921 |
| semaphorin E | AB000220 | D6c | 2949-3181 |
| semaphorin III | L26081 | D6d | 899-1152 |
| semaphorin V | U33920 | D6e | 177-442 |
| SEMAPHORIN-1 | U38276 | D6f | 488-653 |
| TAX1, AXONIN-1/TAQ1 | X85978 | D6g | 209-433 |
| LAR | Y00815 | D6h | 5799-6049 |
| HYALURONAN RECEPTOR (RHAMM) | U29343 | D6i | 2498-2798 |
| PLATELET GLYCOPROTEIN IV (GPV) (GPIIIB) (CD36 ANTIGEN) (PAS IV) (PAS-4 PROTEIN) | M24795 | | |
| caveolin-2 | AF035752 U32114 | D6j | 554-806 |
| caveolin-1 | Z18951 S49856 | D6k | 1340-1519 |
| ANGIOGENESIS REGULATORS | | D6l | 62-413 |
| VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (VEGFR-2) (KDR) (KINASE INSERT DOMAIN RECEPTOR) (FRAGMENT) | L04947; [X61656] | | |
| VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (VEGFR-3) (TYROSINE-PROTEIN KINASE RECEPTOR FLT4, CLASS III). | X68203; [X69876; U43143] | D6m | 2686-3053 |
| FL CYTOKINE RECEPTOR PRECURSOR (EC 2.7.1.112) (TYROSINE- PROTEIN KINASE RECEPTOR FLT3) (STEM CELL TYROSINE KINASE 1) (STK-1) (CD135 ANTIGEN). | U02687 | D6n | 4236-4402 |
| TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR (EC 2.7.1.112). | X60957 [S89716] | D7a | 2491-2965 |
| TYROSINE-PROTEIN KINASE RECEPTOR TIE-2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR TEK) (P140 TEK) | L06139 | D7b | 3114-3536 |
| (TUNICA INTERNA ENDOTHELIAL CELL KINASE). | | D7c | 3243-3586 |

TABLE 3 (CONT)

| Cell Cycle/Growth Regulators | GenBank # | Array Coordinate | Position |
|--|--|------------------|-----------|
| VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) + VEGF RELATED FACTOR ISOFORM VRF186 PRECURSOR | U48801; [U43368] | D7d | 158-648 |
| VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C) (VASCULAR ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRP) (FLT4 LIGAND). | U43142 | D7e | 1165-1559 |
| PLACENTA GROWTH FACTORS 1 AND 2 PRECURSOR (PLGF-1 / PLGF-2). | X54936 | D7f | 1098-1371 |
| SL CYTOKINE PRECURSOR (FLT3/FLK2 LIGAND). | U04806; [U03859] | D7g | 29-362 |
| angiopoietin-1 | U83508 | D7h | 1749-2031 |
| CYSTEINE-RICH FIBROBLAST GROWTH FACTOR RECEPTOR [Golgi membrane sialoglycoprotein MG160 (GLG1)] | U28811; [U64791] | D7i | 3279-4140 |
| FGFR3 (FLG-2) | M58051; [X58255] | D7j | 323-896 |
| FGFR4 | L03840 | D7k | 1503-1743 |
| FIBROBLAST GROWTH FACTOR RECEPTOR 2 PRECURSOR (FGFR-2) (EC 2.7.1.112) (KERATINOCYTE GROWTH FACTOR RECEPTOR) (FGFR2) (BEK) (BFR-1) (K-SAM-1) + K-SAM; K-SAM-III; K-SAM-IV | U11814; [M80634; X52832; M35718; M87771; M87772] | D7l | 753-1189 |
| VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 PRECURSOR (EC 2.7.1.112) (VEGFR-1) (TYROSINE-PROTEIN KINASE RECEPTOR FLT) (FLT-1) (SFLT) | U01134; [X51602] | D7m | 1288-1604 |
| HOMEBOX PROTEIN HOX-D3 [HOX 4A] | D11117 | D7n | 4200-4447 |
| QUADRANT E | | | |
| INVASION REGULATORS | | | |
| MMP-1 (collagenase-1) | X05231 | E1a | 512-836 |
| MMP-2 (gelatinase A) | J03210; [J05471] | E1b | 477-778 |
| MMP-3 (stromelysin-1) | X05232 | E1c | 331-1491 |
| MMP-7 (matrilysin) | X07819 | E1d | 335-738 |
| MMP-8 (collagenase-2) | J05556 | E1e | 532-865 |
| MMP-9 (gelatinase B) | J05070; [D10051] | E1f | 1012-1346 |
| MMP-10 (stromelysin-2) | X07820; [M30461] | E1g | 387-1319 |
| MMP-11 (stromelysin-3) | X57766 | E1h | 263-1508 |
| MMP-12 (matrilysin-2) | L23808 | E1i | 275-787 |
| MMP-13 (collagenase-3) | X75308 | E1j | 463-761 |
| MMP-14 (MT1-MMP) | D26512; [X83535] | E1k | 413-749 |
| MMP-15 (MT2-MMP) | Z48482 | E1l | 1210-1456 |
| MMP-16 (MT3-MMP) | D50477 | E1m | 991-1228 |
| MMP-17 (MT4-MMP) | X89576 | E1n | 630-1830 |
| MMP-19 | X92521 | E2a | 1383-1655 |

TABLE 3 (CONT)

| Cell Cycle/Growth Regulators | GenBank # | Array Coordinate | Position |
|---|--------------------------|------------------|-----------|
| TIMP-1 (erythroid potentiating activity, EPA) | X03124 | E2b | 194-492 |
| TIMP-2 (Ml) | J05593 | E2c | 403-694 |
| TIMP-3 (mitogen-inducible gene 5, mig-5) | Z30183 | E2d | 346-587 |
| TIMP-4 | U76456 | E2e | 445-671 |
| extracellular matrix metalloproteinase inducer EMMPRIN | L20471 | E2f | 23-354 |
| UROKINASE-TYPE PLASMINOGEN ACTIVATOR PRECURSOR (EC 3.4.21.73) (UPA) (U-PLASMINOGEN ACTIVATOR) | M15476 | E2g | 824-1120 |
| TISSUE-TYPE PLASMINOGEN ACTIVATOR PRECURSOR (EC 3.4.21.68) (T-PA) (T-PLASMINOGEN ACTIVATOR) | M15518; [X07393; M18182] | E2h | 1221-1577 |
| PLASMINOGEN PRECURSOR (EC 3.4.21.7) | X05199 | E2i | 1859-2162 |
| PLASMINOGEN ACTIVATOR INHIBITOR-1 PRECURSOR, | X04429 | E2j | 1195-1342 |
| ENDOTHELIAL (PAI-1) | | | |
| PLASMINOGEN ACTIVATOR INHIBITOR-2, PLACENTAL (PAI-2) | M18082; [J02685] | E2k | 378-954 |
| (MONOCYTE ARG- SERPIN) (UROKINASE INHIBITOR). | | | |
| PLASMA SERINE PROTEASE INHIBITOR PRECURSOR (PCI) | M68516; [J02639] | E2l | 8035-8423 |
| (PROTEIN C INHIBITOR) (PLASMINOGEN ACTIVATOR INHIBITOR-3) (PAI3). | | | |
| UROKINASE PLASMINOGEN ACTIVATOR SURFACE RECEPTOR, GPI-ANCHORED FORM PRECURSOR (U-PAR) (MONOCYTE ACTIVATION ANTIGEN MO3) (CD87 ANTIGEN) | U08839 [M83246; X51675] | E2m | 749-1043 |
| LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MACROGLOBULIN RECEPTOR) (A2MR) | X13916 | E2n | 5439-5742 |
| LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2 (MEGALIN) (GLYCOPROTEIN 330) (FRAGMENT) | U04441 | E3a | 1365-2162 |
| ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M) | M11313 | E3b | 3972-4325 |
| PLATELET BASIC PROTEIN PRECURSOR (PBP) (CONTAINS: CONNECTIVE-TISSUE ACTIVATING PEPTIDE III (CTAP-III), LOW-AFFINITY PLATELET FACTOR IV (LA-PF4), BETA-THROMBOGLOBULIN (BETA-TG), NEUTROPHIL-ACTIVATING PEPTIDE 2 (NAP-2)) | M54995; M38441 | E3c | 63-252 |
| ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN PRECURSOR (ALPHA-2-MRAP) (LOW DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN- ASSOCIATED PROTEIN 1) (RAP) | M63959 | E3d | 440-890 |
| NUCLEOSIDE DIPHOSPHATE KINASE A (EC 2.7.4.6) (NDK A) (NDP KINASE A) (TUMOR METASTATIC PROCESS-ASSOCIATED PROTEIN) (METASTASIS INHIBITION FACTOR NM23) (NM23-H1). | X17620 | E3e | 245-612 |

TABLE 3 (CONT)

| Cell Cycle/Growth Regulators | GenBank # | Array Coordinate | Position |
|---|---------------------------------|------------------|-----------|
| NUCLEOSIDE DIPHOSPHATE KINASE B (EC 2.7.4.6) (NDK B) (NDP KINASE B) (NM23-H2) (C-MYC PURINE-BINDING TRANSCRIPTION FACTOR PUF) | L16785; [M36981] | E3f | 69-351 |
| nm23-H4; NUCLEOSIDE-DIPHOSPHATE KINASE (EC 2.7.4.6) (NUCLEOSIDE 5'-DIPHOSPHATE PHOSPHOTRANSFERASE) (NDK) | Y07604 | E3g | 141-448 |
| malignant melanoma metastasis-suppressor (KiSS-1) gene | U43527 | E3h | 116-454 |
| METASTASIS-ASSOCIATED MTA1 | U35113 | E3i | 957-1825 |
| PROSTATE-SPECIFIC MEMBRANE ANTIGEN (PSM) | M99487 | E3j | 1068-1200 |
| metalloproteinase/disintegrin/cysteine-rich protein precursor (MDC9) | U41766 | E3k | 640-958 |
| RHO FAMILY SMALL GTPASES AND THEIR REGULATORS | | | |
| rhoB | X06820 | E3l | 53-1648 |
| rhoC (H9); SMALL GTPase (rhoC) | L25081 | E3m | 637-1473 |
| rhoG | X61587 | E3n | 900-1228 |
| Rho6 protein | Y07923 | E4a | 33-388 |
| Rho7 protein | X95456 | E4b | 75-377 |
| Rho8 protein | X95282 | E4c | 209-534 |
| RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 (P21-RAC1) | M29870; [M31467] | E4d | 55-429 |
| (RAS-LIKE PROTEIN TC25) | M64595; [M29871] | E4e | 31-1185 |
| RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 (P21-RAC2) | M31470 | E4f | 80-350 |
| ras-like protein TC10 | Z35227 | E4g | 491-759 |
| ras-like small GTPase TTF | D85815 | E4h | 130-361 |
| rhoHP1 | U43195 | E4i | 3793-4233 |
| Rho-associated, coiled-coil containing protein kinase p160ROCK | U02570 | E4j | 864-1182 |
| CDC42 GTPase-activating protein | U82532 | E4k | 309-554 |
| GDI-dissociation inhibitor RhoGDIgamma | U16296 | E4l | 4275-4645 |
| T-lymphoma invasion and metastasis inducing TIAM1 | U11690 | | |
| PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR(RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN) | X78817 | E4m | 3033-4165 |
| RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131) | L20688 | E4n | 781-1170 |
| rho GDP-dissociation inhibitor protein 2 (Ly-GDI) | X69550 | E5a | 322-600 |
| rho GDP-dissociation inhibitor 1 | U24152 | E5b | 328-624 |
| SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA (EC 2.7.1.-) (P65-PAK) (P21- ACTIVATED KINASE) (ALPHA-PAK) | | E5c | 756-1055 |
| p21-activated protein kinase (Pak2) | U24153 | E5d | 335-671 |
| CELL CELL INTERACTION | | | |
| CADHERIN-2 (N-CADHERIN) | M34064 [X57548; X54315; S42303] | | |
| CADHERIN-3 PLACENTAL-CADHERIN PRECURSOR (P-CADHERIN) | X63629 | E5e | 942-1299 |
| | | E5f | 542-835 |

TABLE 3 (CONT)

| Cell Cycle/Growth Regulators | GenBank # | Array Coordinate | Position |
|--|--------------------------------|------------------|-----------|
| CADHERIN-4 RETINAL-CADHERIN PRECURSOR (R-CADHERIN) (R-CAD) | L34059 | E5g | 1172-1425 |
| CADHERIN-5 VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (7B4 ANTIGEN) (CD144 ANTIGEN). | X79981; [X59796] | E5h | 1607-1769 |
| CADHERIN-6 | D31784 | E5i | 2119-2443 |
| CADHERIN-8 | L34060 | E5j | 1069-1347 |
| CADHERIN-11 (OSTEOBLAST-CADHERIN) (OB-CADHERIN) | L34056 | E5k | 1778-2076 |
| CADHERIN-12 (BR-CADHERIN) (N-CADHERIN 2) (CADHERIN, NEURAL TYPE, 2) | L34057; [L33477] | E5l | 657-903 |
| CADHERIN-13 T-CADHERIN PRECURSOR (TRUNCATED-CADHERIN) (H-CADHERIN) (HEART-CADHERIN) | L34058; [U59289; U59288] | E5m | 949-1187 |
| CADHERIN-14 MUSCLE-CADHERIN PRECURSOR (M-CADHERIN) (CADHERIN-14) (CADHERIN-15) | D83542 | E5n | 228-456 |
| ALPHA-CATENIN (CADHERIN-ASSOCIATED PROTEIN) (ALPHA E-CATENIN) | D13866 [D14705 L23805; L22080] | E6a | 55-492 |
| BETA-CATENIN | M94151 | E6b | 2296-2545 |
| PLAKOGLOBIN (DESMOPLAKIN III) | X87838 [Z19054] | E6c | 2061-2463 |
| APC (DP2.5) | M23410 | E6d | 2000-2312 |
| neuroendocrine-dlg (NE-dlg) a novel human homolog of the Drosophila discs large (dlg) tumor suppressor protein interacting with the APC protein | M74088; [M73548] | E6e | 7992-8326 |
| EB1, a protein that binds to APC | U24166 | E6f | 2210-3116 |
| protocadherin 42 | L11370 | E6g | 488-796 |
| protocadherin 43 | L11373 | E6h | 1246-1605 |
| desmoplakin I | M77830 | E6i | 1018-1388 |
| envoplakin (EVPL) | U53786 | E6j | 6987-7828 |
| bullous pemphigoid antigen | M63618 | E6k | 5583-5788 |
| desmoglein 2 | Z26317 [S64273] | E6l | 5680-6055 |
| desmoglein type 1 | X56654 | E6m | 2819-3135 |
| desmoglein type 1 | X72925 | E6n | 2578-2889 |
| desmoglein type 3 + desmoglein type 4 | X83929; [D17427] | E7a | 475-1154 |
| DSC2 mRNA for desmocolins type 2a and 2b | X56807 | E7b | 608-1607 |
| EPHRIIN-A1 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 1) (LERK-1) (IMMEDIATE EARLY RESPONSE PROTEIN B61) (TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 4). | M57730 M37476 | E7c | 802-1115 |
| EPHRIIN-A5 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 7) (LERK-7) (AL-1). | U26403 | E7d | 124-1062 |
| | | E7e | 375-1325 |

TABLE 3 (CONT)

| Cell Cycle/Growth Regulators | GenBank # | Array Coordinate | Position |
|---|------------------|------------------|-------------|
| EPHRIN-B1 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 2) (LERK-2) (ELK LIGAND PRECURSOR) (ELK-L). | U09304 | E7i | 507-1186 |
| EPHRIN-B2 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 5) (LERK-5) (HTK LIGAND) (HTK-L). | L38734 | E7g | 442-560 |
| EPHRIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 8) (LERK-8) (EPH-RELATED RECEPTOR TRANSMEMBRANE LIGAND ELK-L3). | U66406 | | 2056-2282 |
| EPHRIN TYPE-A RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ECK) (EPITHELIAL CELL KINASE). | M59371 M36395 | E7h | 249-1426 |
| EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-1) (EPH HOMOLOG Y KINASE-1) (RECEPTOR PROTEIN- TYROSINE KINASE HEK7). | X95425 | E7i | 644-1300 |
| EPHRIN TYPE-B RECEPTOR 1 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EPH-2) (NET). | L40636 | E7k | 998-1469 |
| EPHRIN TYPE-B RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN EPH-3) (DRT) | L41939 | E7l | 454-1225 |
| EPHRIN TYPE-B RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR HTK). | U07695 | E7m | 758-1652 |
| TYROSINE-PROTEIN KINASE HCK (EC 2.7.1.112) (P59-HCK AND P60-HCK) (HEMOPOIETIC CELL KINASE). | M16591 | E7n | 194-1187 |
| | | | |
| | | | |
| QUADRANT F | | | |
| GROWTH FACTORS/CYTOKINES | | | |
| AMPHIREGULIN | M30704 | F1a | 511-837 |
| BCGF1 (B-cell growth factor) | M15530 | F1b | 13-248 |
| BDNF | M61176 | F1c | 982-1265 |
| BETA NGF | X52599 | F1d | 360-1339 |
| VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF). | M32977; [M27281] | F1e | 198-622 |
| BIGH3 | M77349 | F1f | 705-1703 |
| BONE MORPHOGENETIC PROTEIN 1 (procollagen C-proteinase) (pCP-2) | M22488; [U50330] | F1g | 702-1098 |
| BONE MORPHOGENETIC PROTEIN 2A | M22489 | F1h | 567-997 |
| BONE MORPHOGENETIC PROTEIN 3 | M22491 | F1i | 1458-1731 |
| BONE MORPHOGENETIC PROTEIN 3B | D49493 | F1j | 16188-16418 |
| BONE MORPHOGENETIC PROTEIN 4 (BMP-2B) | D30751; [M22490] | F1k | 943-1321 |
| BONE MORPHOGENETIC PROTEIN 5 | M60314 | F1l | 1679-1982 |

TABLE 3 (CONT)

| Cell Cycle/Growth Regulators | GenBank # | Array Coordinate | Position |
|--|-----------------------------|------------------|-----------|
| BONE MORPHOGENETIC PROTEIN 6 | M60315 | F1m | 1067-1327 |
| BONE MORPHOGENETIC PROTEIN 7 (OSTEOGENIC PROTEIN 1) | M60316 | F1n | 451-691 |
| BONE MORPHOGENETIC PROTEIN 8 (OSTEOGENIC PROTEIN 2) | M97016 | F2a | 1345-1645 |
| BPGF-1 | L42379 | F2b | 825-1213 |
| ONTF, ISOFORM B AND C | A26792 | F2c | 213-448 |
| CONNECTIVE TISSUE GROWTH FACTOR | M92934 | F2d | 1459-1748 |
| EGF (kidney) | X04571 | F2e | 4164-4434 |
| EGF-LIKE GROWTH FACTOR | M60278 | F2f | 1905-2146 |
| endothelin 2 | M65189 | F2g | 338-570 |
| endothelin 3 | J05081 | F2h | 1428-1685 |
| HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA- ENDOTHELIAL CELL GROWTH FACTOR) (ECGF, BETA). | X51943; [M13361; X65778] | | |
| FGF2; HEPARIN-BINDING GROWTH FACTOR 2 PRECURSOR (PROSTATROPIN). (HBGF-2) (BASIC FIBROBLAST GROWTH FACTOR) (BFGF) (PROSTATROPIN) | M27968 | F2i | 1131-1502 |
| FGF-3; INT-2 PROTO-ONCOGENE PROTEIN PRECURSOR (FIBROBLAST GROWTH FACTOR-3)(HBGF-3). | X14445 | F2j | 1384-1646 |
| FGF-5; FIBROBLAST GROWTH FACTOR-5 PRECURSOR (HBGF-5). | M37825 | F2k | 189-940 |
| FGF-6; FIBROBLAST GROWTH FACTOR-6 PRECURSOR (HBGF-6) (HST-2). | X63454 | F2l | 603-1086 |
| FGF-7; KERATINOCYTE GROWTH FACTOR PRECURSOR (KGF) (FIBROBLAST GROWTH FACTOR-7) (HBGF-7). | M60828 | F2m | 287-456 |
| FGF-8; ANDROGEN-INDUCED GROWTH FACTOR PRECURSOR (AIGF) (HBGF-8) (FIBROBLAST GROWTH FACTOR-8) | U36223 | F2n | 522-955 |
| FGF-9; GLIA-ACTIVATING FACTOR PRECURSOR (GAF) (FIBROBLAST GROWTH FACTOR-9) (HBGF-9). | D14838 | F3a | 32-3106 |
| FHF-1 | U66197 | F3b | 110-949 |
| GDNF | L19083 | F3c | 17-566 |
| GLIA MATURATION FACTOR beta | HG563 [M86492; AB001106] | F3d | 248-390 |
| RECOMBINANT GLIAL GROWTH FACTOR + NEU DIFFERENTIATION FACTOR + HEREGLIN | L12260; U02326; M94165 | F3e | 203-434 |
| TRANSFORMING GROWTH FACTOR-BETA-2 (glioblastoma-derived t- cell suppressor factor) | M19154; [Y00083] | F3f | 1069-1452 |
| GROWTH INHIBITORY FACTOR (METALLOTHIONEIN-III) (MT-III) | D13365; [M93311] | F3g | 1538-1878 |
| | | F3h | 4-1052 |

TABLE 3 (CONT)

| Cell Cycle/Growth Regulators | GenBank # | Array Coordinate | Position |
|---|--------------------------|------------------|-----------|
| PLEIOTROPHIN PRECURSOR (PTN) (HEPARIN-BINDING GROWTH-ASSOCIATED MOLECULE) (HB-GAM) (HEPARIN-BINDING GROWTH FACTOR 8) (HBGF-8) (OSTEOBLAST SPECIFIC FACTOR 1) (OSF-1) (HEPARIN-BINDING NEURITE OUTGROWTH PROMOTING FACTOR 1) (HBNF-1). | M57399; [X52946; D80226] | F3j | 602-847 |
| EARLY GROWTH RESPONSE PROTEIN 1 (EGR-1) (KROX24) (TRANSCRIPTION FACTOR ETR103) (ZINC FINGER PROTEIN 225) (AT225). | M62829; [X52541] | F3j | 989-1276 |
| HEPATOCYTE GROWTH FACTOR-LIKE (macrophage-stimulating protein (MST1)) | M74178 | F3k | 1643-2015 |
| HEPTOMA-DERIVED GROWTH FACTOR | D16431 | F3l | 359-625 |
| HEPATOCYTE GROWTH FACTOR PRECURSOR (SCATTER FACTOR) (SF) (HEPATOPOEITIN A). | M60718 | F3m | 1549-1970 |
| HGF AGONIST/ANTAGONIST | U46010 | F3n | 895-1051 |
| COMPETITIVE HEPATOCYTE GROWTH FACTOR ANTAGONIST. AN ALTERNATIVE TRANSCRIPT OF THE HEPATOCYTE GROWTH FACTOR PRECURSOR (SCATTER FACTOR) (SF) (HEPATOPOEITIN A) | M77227 | | |
| IFN-GAMMA ANTAGONIST CYTOKINE | A25270 | F4a | 947-1968 |
| IGF-1 | M27544; [M37484] | F4b | 395-685 |
| INTERLEUKIN 1 RECEPTOR ANTAGONIST | M63099 | F4c | 652-919 |
| INTERLEUKIN 6 RECEPTOR | M20566 | F4d | 225-1294 |
| INTERLEUKIN IL-1 ALPHA | X02851 | F4e | 2359-2823 |
| INTERLEUKIN IL-1BETA | K02770 | F4f | 1107-1473 |
| INTERLEUKIN IL-2 | A14844 | F4g | 917-1208 |
| INTERLEUKIN-3 PRECURSOR (IL-3) (MULTIPOTENTIAL COLONY-STIMULATING FACTOR) (HEMATOPOIETIC GROWTH FACTOR) (P-CELL STIMULATING FACTOR) (MAST-CELL GROWTH FACTOR) (MCGF) (IL3). | M14743; [M17115] | F4h | 181-436 |
| INTERLEUKIN IL-4 | M13982 | F4i | 390-608 |
| INTERLEUKIN IL-5 (B CELL DIFFERENTIATION FACTOR 1) (T-CELL REPLACING FACTOR) (EOSINOPHIL DIFFERENTIATION FACTOR) | X04688; [J03478] | F4j | 216-459 |
| INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR). | X04602; [M14584] | F4k | 35-279 |
| INTERLEUKIN IL-7 | J04156 | F4l | 130-555 |
| INTERLEUKIN IL-9 (P40) | X17543; [M30134] | F4m | 174-447 |
| INTERLEUKIN IL-10 | M57627 | F4n | 156-399 |
| INTERLEUKIN IL-11 [adipogenesis inhibitory factor] | M57765 | F5a | 442-648 |
| INTERLEUKIN IL-12 (NKSF, P35) | M65291 | F5b | 132-460 |
| | | F5c | 600-990 |

TABLE 3 (CONT)

| Cell Cycle/Growth Regulators | GenBank # | Array Coordinate | Position |
|---|---------------------------|------------------|-----------|
| INTERLEUKIN IL-12 (NKSFP40) | M65290 | F5d | 622-848 |
| INTERLEUKIN IL-13 | L06801 | F5e | 285-743 |
| INTERLEUKIN IL-14 | L15344 | F5i | 1181-1562 |
| INTERLEUKIN IL-15 | U14407 | F5g | 338-695 |
| INTERLEUKIN IL-17 | U32659 | F5h | 257-578 |
| LEUKOCYTE INTERFERON ALPHA | J00209; [J00207] | F5i | 89-430 |
| LEUKOCYTE INTERFERON BETA 1 | M28622 | F5j | 345-730 |
| LEUKOCYTE INTERFERON GAMMA | X01992 | F5k | 391-586 |
| LEUKOCYTE INTERFERON-INDUCIBLE PEPTIDE | X02492 | F5l | 372-550 |
| LIF | X13967; [M63420] | F5m | 1810-2239 |
| MIF | M25639 | F5n | 256-476 |
| NEURITE PROMOTING FACTOR(NEXIN), glia derived | A03911 | F6a | 667-915 |
| NT-3 (NEUROTROPHIN-3 PRECURSOR) (NEUROTROPHIC FACTOR) | X53655; [M37763] | F6b | 112-416 |
| (HDMF) (NERVE GROWTH FACTOR 2) (NGF-2). | M86528; S41541; [S41540]; | F6c | 721-1079 |
| NT-4 (NT-5) + NT-6 | S41522 | F6d | 255-1326 |
| PDGF assoc. protein | U41745 | F6e | 522-955 |
| PLATELET-DERIVED GROWTH FACTOR A CHAIN | X06374 | F6f | 1663-2125 |
| PLATELET-DERIVED GROWTH FACTOR, B CHAIN PRECURSOR | X02811; [X02744 ; | F6g | 346-1241 |
| (PDGF B-CHAIN) (PDGF-2) (BACAPLERMIN) (C-SIS) | M12783] | F6h | 1053-1481 |
| SDF1A (pre-B cell stimulating factor homologue) | L36034 | F6i | 898-1283 |
| SDF1B | U16752; [L36033] | F6j | 273-504 |
| STEM CELL FACTOR (C-KIT LIGAND) | M59964 | | |
| T CELL RECEPTOR VARIABLE REGION | M21626 | | |
| TDGF1 (TERATOCARCINOMA-DERIVED GROWTH FACTOR 1) | M96956; [M96955] | | |
| (EPIDERMAL GROWTH FACTOR)-LIKE CRIPTO PROTEIN CR1) | | | |
| (CRIPTO-1 GROWTH FACTOR) (CRGF) + TDGF2 | | | |
| (TERATOCARCINOMA-DERIVED GROWTH FACTOR 2) (EPIDERMAL | | | |
| GROWTH FACTOR-LIKE CRIPTO PROTEIN CR3) (CRIPTO-3 GROWTH | | | |
| TGF-b superfamily receptor type I (ALK-1) (SRK3) | L17075 | F6k | 1294-1712 |
| TGF-BETA3 | J03241 | F6l | 814-1077 |
| THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY | L36052; [L36051; U11025] | F6m | |
| STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE | | | |
| GROWTH AND DEVELOPMENT FACTOR) (MGDF) (THPO) | | | |
| TRANSFORMING GROWTH FACTOR-ALPHA | K03222 | F6n | 1416-1833 |
| TRANSFORMING GROWTH FACTOR-BETA | X02812 | F7a | 338-595 |
| CD27 (CD70 ANTIGEN) | L08096; [S69339] | F7b | 2398-2575 |
| CD30 | L09753 | F7c | 233-627 |
| CD40 | L07414 | F7d | 627-1019 |
| | | F7e | 863-1277 |

TABLE 3 (CONT)

[illegible]

Apoptosis Array

In the apoptosis array according to the subject invention, all of the unique polynucleotide probe compositions correspond to genes that are associated with apoptosis, e.g. cell cycle genes. In a specific apoptosis array of interest, the spots are as provided in

5 Table 4.

TABLE 4

| GenBank # | Cell Cycle - Gene Name | Array Coordinate |
|------------------|--|------------------|
| X05360 | CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.-) (P34 PROTEIN KINASE) (CYCLIN-DEPENDENT KINASE 1) (CDK1) | 3B |
| M68520 | CELL DIVISION PROTEIN KINASE 2 (EC 2.7.1.-) (P33 PROTEIN KINASE) | 3C |
| X66357 | CELL DIVISION PROTEIN KINASE 3 (EC 2.7.1.-) | 3D |
| M14505 | CELL DIVISION PROTEIN KINASE 4 (EC 2.7.1.-) (PSK-J3) | 3E |
| X66364 | CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE). | 3F |
| X66365 | CELL DIVISION PROTEIN KINASE 6 (EC 2.7.1.-) (KINASE PLSTIRE) | 3G |
| L20320 | CELL DIVISION PROTEIN KINASE 7 (EC 2.7.1.-) (CDK-ACTIVATING KINASE) (CAK) (39 KD PROTEIN KINASE) (P39 MO15) (STK1) (CAK1). | 3H |
| U34051 | CYCLIN-DEPENDENT KINASE 5 ACTIVATOR ISOFORM P39I PRECURSOR (CDK5 ACTIVATOR) (P39I). | 3I |
| X80343 | CYCLIN-DEPENDENT KINASE 5 ACTIVATOR PRECURSOR (CDK5 ACTIVATOR) (TAU PROTEIN KINASE II 23 KD SUBUNIT) (TPKII REGULATORY SUBUNIT) (P23) (P25) (P35). | 3J |
| M81933 | CDC25A; M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) | 3K |
| M81934; [S78187] | CDC25B; M-PHASE INDUCER PHOSPHATASE 2 (EC 3.1.3.48). (CDC25HU2) | 3L |
| M34065 | CDC25C; M-PHASE INDUCER PHOSPHATASE 3 (EC 3.1.3.48). | 3M |
| L29222 | CLK-1 | 3N |
| L29216 | CLK-2 | 3O |
| L29220 | CLK-3 | 4B |
| X66358 | SERINE/THREONINE-PROTEIN KINASE KIALRE | 4C |
| X66363 | SERINE/THREONINE-PROTEIN KINASE PCTAIRE-1 | 4D |
| X66360 | SERINE/THREONINE-PROTEIN KINASE PCTAIRE-2 | 4E |
| X66362 | SERINE/THREONINE-PROTEIN KINASE PCTAIRE-3 | 4F |
| L25676 | SERINE/THREONINE-PROTEIN KINASE PITALRE | 4G |
| M80629 | CDC2-RELATED PROTEIN KINASE CHED | 4H |
| L33264 | CDC2-RELATED KINASE PISSLRE | 4I |
| X51688 | CYCLIN A | 4J |
| M25753 | CYCLIN B1 G2/MITOTIC-SPECIFIC | 4K |
| M74091 | CYCLIN C G1/S-SPECIFIC | 4L |
| X59798; [M64349] | CYCLIN D1 (CYCLIN PRAD1) (BCL-1 ONCOGENE) | 4M |
| D13639 [M90813] | CYCLIN D2 | 4N |
| M92287 | CYCLIN D3 | 4O |
| M73812 | CYCLIN E | 5B |
| U47413 [L49504] | CYCLIN G1 | 5C |

TABLE 4 (CONT)

| GenBank # | Cell Cycle - Gene Name | Array Coordinate |
|------------------|--|------------------|
| U47414 [L49506] | CYCLIN G2 | 5D |
| U11791 [U12685] | CYCLIN H | 5E |
| | CYCLIN-DEPENDENT KINASE INHIBITOR 1 (MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN 6) (MDA-6) (P21) (CDK-INTERACTING PROTEIN 1) (CIP1) (WAF1) (CDKN1A) (CDKN1) (SDI1) (PIC1) (CAP20) | 5F |
| U09579; [L25610] | CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITOR P57) (P57KIP2) | 5G |
| U22398 | CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A) | 5H |
| L27211 | (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). (CDKN2A) | 5I |
| | CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B) (MULTIPLE TUMOR SUPPRESSOR 2) (MTS2) (CDKN2B). | 5J |
| U17075; [L36844] | CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D). | |
| U40343; [U20498] | CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1 (RING FINGER PROTEIN MAT1) (MENAGE A TROIS) (CDK7/CYCLIN H ASSEMBLY FACTOR) (P38) (P35 (MNAT1) (MAT1) (CAP35). | 5K |
| X92669; [X87843] | WEE1-LIKE PROTEIN KINASE (EC 2.7.1.112) (WEE1HU) | 5L |
| U10564 | SERINE/THREONINE-PROTEIN KINASE PLK (EC 2.7.1.1) (PLK-1) (STPK13) | 5M |
| U01038 | PHOSPHOLIPASE D1 | 5N |
| U38545 | NEDD5 PROTEIN HOMOLOG. | 5O |
| D63878 | CDC10 PROTEIN HOMOLOG | 6B |
| S72008 | CDC27HS PROTEIN | 6C |
| U00001 | UBIQUITIN-CONJUGATING ENZYME E2-CDC34 | 6D |
| L22005 | CDC16HS. | 6E |
| U18291 | CDC37 HOMOLOG. | 6F |
| U63131 | CDC6-RELATED PROTEIN | 6G |
| U77949 | EXTRACELLULAR SIGNAL-REGULATED KINASE 1 (EC 2.7.1.1) (ERK1) (INSULIN-STIMULATED MAP2 KINASE) (MAP KINASE 1) (MAPK 1) (P44-ERK1) (ERT2) (P44-MAPK) (MICROTUBULE-ASSOCIATED PROTEIN-2 KINASE). | 6H |
| X60188 | EXTRACELLULAR SIGNAL-REGULATED KINASE 2 (EC 2.7.1.1) (ERK2) (MITOGEN-ACTIVATED PROTEIN KINASE 2) (MAP KINASE 2) (MAPK 2) (P42-MAPK) (ERT1). | 6I |
| M84489 | EXTRACELLULAR SIGNAL-REGULATED KINASE 3 (EC 2.7.1.1) (ERK3) (MAP KINASE ISOFORM P97) (P97-MAPK). | 6J |
| X80692 | EXTRACELLULAR SIGNAL-REGULATED KINASE 4 (EC 2.7.1.1) (ERK4) (MAP KINASE ISOFORM P63) (P63-MAPK). | 6K |
| X59727 | EXTRACELLULAR SIGNAL-REGULATED KINASE 5 (EC 2.7.1.1) (ERK5) (ERK4) (BMK1 KINASE) | 6L |
| U25278 | | |

TABLE 4 (CONT)

| GenBank # | Cell Cycle - Gene Name | Array Coordinate |
|------------------|---|------------------|
| X79483 | EXTRACELLULAR SIGNAL-REGULATED KINASE 6 (EC 2.7.1.-) (ERK5) (ERK5) | 6M |
| | MITOGEN-ACTIVATED PROTEIN KINASE P38 (EC 2.7.1.-) (MAP KINASE P38) | |
| | (CYTOKINE SUPPRESSIVE ANTI-INFLAMMATORY DRUG BINDING PROTEIN) | |
| | (CSAID BINDING PROTEIN) (CSBP) (MAX-INTERACTING PROTEIN 2) (MAP KINASE MXI2) | 6N |
| L35253; [L35263] | STRESS-ACTIVATED PROTEIN KINASE JNK1 (EC 2.7.1.-) (C-JUN N-TERMINAL KINASE 1) (JNK-46) | 6O |
| L26318 | STRESS-ACTIVATED PROTEIN KINASE JNK2 (EC 2.7.1.-) (C-JUN N-TERMINAL KINASE 2) (JNK-55) | 7B |
| L31951 | STRESS-ACTIVATED PROTEIN KINASE JNK3 (EC 2.7.1.-) (C-JUN N-TERMINAL KINASE 3) (JNK3) (MAP KINASE P49 3F12) | 7C |
| U34819; [U07620] | DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 5 (EC 2.7.1.-) (MAP KINASE KINASE 5) (MAPKK 5) (MAP/ERK KINASE 5) | 7D |
| U25265 | DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (EC 2.7.1.-) (MAP KINASE KINASE 1) (MAPKK 1) (ERK ACTIVATOR KINASE 1) (MAPK/ERK KINASE 1) (MEK1) | 7E |
| L05624 | DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 6 (EC 2.7.1.-) (MAP KINASE KINASE 6) (MAPKK 6) (MAP/ERK KINASE 6) (SAPKK3) | 7F |
| U39657 | MEK KINASE 3 | 7G |
| U78876 | PCNA (CYCLIN) | 7H |
| M15796; [J04718] | PIN1 | 7I |
| U49070 | RETINOBLASTOMA-ASSOCIATED PROTEIN [RETINOBLASTOMA SUSCEPTIBILITY] | 7J |
| M15400 | RB2/P130 | 7K |
| X74594 | RB2/P48 | 7L |
| X74262 | RB2 RETINOBLASTOMA BINDING PROTEIN | 7M |
| S66431 | RB1(RETINOBLASTOMA-BINDING PROTEIN) | 7N |
| S57153; S57160 | RBQ1 RETINOBLASTOMA BINDING PROTEIN | 7O |
| X85133 | RBQ-3 | 8B |
| X85134 | E2F-1 PRB-BINDING PROTEIN | 8C |
| M96577 | E2F-3 | 8D |
| Y10479 | E2F-5 | 8E |
| U15642 | E2F-RELATED TRANSCRIPTION FACTOR (DP-1) | 8F |
| L23959 | DP2 (HUMDP2), DIMERIZATION PARTNER OF E2F | 8G |
| U18422 | ABL INTERACTOR 2 (ABI-2) + ABL BINDING PROTEIN 3 (ABLP3) [ARGBP1B] | 8H |
| U23435; U31089 | GRB2 [GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2] | 8I |
| L29511 | | |

TABLE 4 (CONT)

| GenBank # | Cell Cycle - Gene Name | Array Coordinate |
|-------------------|---|------------------|
| U69276 | GRB-IR / GRB10 | 8J |
| X03484 | RAF ONCOGENE | 8K |
| M95712 | RAF-B- | 8L |
| J04111 | TRANSCRIPTION FACTOR AP-1 [C-JUN PROTO ONCOGENE] | 8M |
| M29039 | JUN B TRANSACTIVATOR | 8N |
| X56681 | TRANSCRIPTION FACTOR JUN-D | 8O |
| M13228 | N-MYC | 9B |
| D89667 | C-MYC BINDING PROTEIN | 9C |
| L16785 | NUCLEOSIDE DIPHOSPHATE KINASE B [C-MYC TRANSCRIPTION FACTOR (PUF)] | 9D |
| X16416 [M14752] | c-abl | 9E |
| | | |
| | p53 PATHWAY | |
| M14694 | CELLULAR TUMOR ANTIGEN P53 | 9F |
| Z12020 | MDM2 PROTEIN (P53-ASSOCIATED PROTEIN) + MDM2-A (GB: U33199) + MDM2-C (GB: U33201) | 9G |
| AF007111 | MDM2-LIKE P53-BINDING PROTEIN (MDMX) | 9H |
| Y11416 | P73, A MONOALLELICALLY EXPRESSED P53-RELATED PROTEIN | 9I |
| AF010310 AF010311 | P53 INDUCED PROTEIN | 9J |
| AF010309 | PIG3 (PIG3) | 9K |
| AF010312 | PIG7 (PIG7) | 9L |
| AF010314 | PIG10 (PIG10) | 9M |
| AF010315 | PIG11 (PIG11) | 9N |
| AF010316 | PIG12 (PIG12) | 9O |
| U90313 | GLUTATHIONE-S-TRANSFERASE HOMOLOG | 10B |
| U66469 | P53-DEPENDENT CELL GROWTH REGULATOR CGR19 | 10C |
| AF001954 | GROWTH INHIBITOR P33ING1 (ING1) | 10D |
| L13698 | GROWTH-ARREST-SPECIFIC PROTEIN 1 (GAS-1) | 10E |
| | | |
| | BCL FAMILY | |
| M14745 | BCL2 | 10F |
| U58334 | BCL2 AND P53 BINDING PROTEIN BBP/53BP2 (BBP/53BP2) | 10G |
| L22474 | BAX | 10H |
| U59747 | APOPTOSIS REGULATOR BCL-W | 10I |
| L08246 | INDUCED MYELOID LEUKEMIA CELL DIFFERENTIATION PROTEIN MCL-1 (ORF IS AT NT. 61-1053; ML) | 10J |

TABLE 4 (CONT)

| GenBank # | Cell Cycle - Gene Name | Array Coordinate |
|----------------------|--|------------------|
| | BCL2-RELATED PROTEIN A1 (BFL-1 PROTEIN) (HEMOPOIETIC-SPECIFIC EARLY RESPONSE PROTEIN) (GRS PROTEIN) | 10K |
| U29680 | BCL-2 INTERACTING KILLER (APOPTOSIS INDUCER NBK) (BP4) (BIP1) (BIK) | 10L |
| X89986; [U34584] | BCL-2 HOMOLOGOUS ANTAGONIST/KILLER (APOPTOSIS REGULATOR BAK) | 10M |
| U23765; [U16812;] | BCL-2 HOMOLOGOUS ANTAGONIST/KILLER (APOPTOSIS REGULATOR BAK) | 10N |
| S82185 | BRAG-1=BRAIN-RELATED APOPTOSIS GENE/BCL-2 HOMOLOG | 10O |
| U66879 | BAD PROTEIN (BCL-2 BINDING COMPONENT 6) | |
| | BCL-2 BINDING ATHANOGENE-1 (BAG-1) (GLUCOCORTICOID RECEPTOR-ASSOCIATED PROTEIN RAP46). | 11B |
| S83171; [Z35491] | Harakiri, a protein that activates cell death and interacts w. Bcl-2 and Bcl-XL | 11C |
| U76376 | | |
| | CASPASE CASCADE | |
| | CASPASES | |
| U13699; [M87507; X6] | (ICE) (INTERLEUKIN-1 BETA CONVERTING ENZYME) (P45) (CASPASE-1) | 11D |
| U13021; [U13022] | (CASPASE-2) (ICH-1L) (ICH-1S) | 11E |
| | APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CASPASE-3) (CPP32) (YAMA PROTEIN) (CASPASE-3) ISOFORM ALPHA | 11F |
| U13737 | ICH-2 PROTEASE PRECURSOR (EC 3.4.22.-) (TX PROTEASE) (ICEREL-II) (CASPASE-4) + CASPASE-5 PRECURSOR (EC 3.4.22.-) (ICH-3 PROTEASE) (TY PROTEASE (ICEREL-III). | 11G |
| U28014; U28015 | CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) | 11H |
| U20537; U20536 | ISOFORM BETA + ISOFORM ALPHA | |
| | CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) (LICE2) | 11I |
| U37448 | CASPASE-8 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 5) (MORT1-ASSOCIATED CED-3 HOMOLOG) (MACH) (FADD-HOMOLOGOUS ICE/CED-3-LIKE PROTEASE) (FADD-LIKE ICE) (FLICE) (APOPTOTIC CYSTEINE PROTEASE) (APOPTOTIC PROTEASE MCH-5) (CAP4) (CASP8) (MCH5) ISOFORM | 11J |
| U60520; U58143; X98 | CASPASE-8 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 5) (MORT1-ASSOCIATED CED-3 HOMOLOG) (MACH) (FADD-HOMOLOGOUS ICE/CED-3-LIKE PROTEASE) (FADD-LIKE ICE) (FLICE) (APOPTOTIC CYSTEINE PROTEASE) (APOPTOTIC PROTEASE MCH-5) (CAP4) (CASP8) (MCH5) ISOFORM | |
| U60520; U58143; X98 | CASPASE-9 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 6) (ICE-LAP6) (APOPTOTIC PROTEASE MCH-6) | 11K |
| U56390; [U60521] | ICE-LIKE APOPTOTIC PROTEASE 4 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-4) (CASPASE-10) | 11L |
| U60519 | | 11M |

TABLE 4 (CONT)

| GenBank # | Cell Cycle - Gene Name | Array Coordinate |
|----------------------------|---|------------------|
| | CASPASE REGULATORS | |
| L41690 | TNF RECEPTOR-1 ASSOCIATED PROTEIN (TRADD) | 11N |
| U69108 | TRAF5 | 11O |
| U78798; [L81153] | TRAF6 | 12B |
| U59863; [U63830] | TRAF-INTERACTING PROTEIN 1-TRAF (TRAF FAMILY MEMBER-ASSOCIATED NF-KB ACTIVATOR TANK) | 12C |
| U77845 | TRAF-INTERACTING PROTEIN (TRIP) | 12D |
| Y10256 | SERINE/THREONINE PROTEIN KINASE, NIK; BINDS SPECIFICALLY TO TRAF2 | 12E |
| | CASPER, A FADD- AND CASPASE-RELATED INDUCER OF APOPTOSIS [CASH-ALPHA+ CASH-BETA] (FLAME-1) (FLICE-LIKE INHIBITORY PROTEIN) | 12F |
| AF010127; [Y14039; Y14040] | DEATH DOMAIN CONTAINING PROTEIN CRADD, APOPTOTIC ADAPTOR MOLECULE FOR CASPASE-2 AND FASL/TNF RECEPTOR-INTERACTING PROTEIN | |
| U84388 | RIP | 12G |
| U25994; [U50062] | CELL DEATH PROTEIN KINASE RIP | 12H |
| AF015956 | DAXX, A FAS-BINDING PROTEIN THAT ACTIVATES JNK AND APOPTOSIS | 12I |
| | TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN (TRAP3) | |
| U12597 | | 12J |
| U21092; [U15637; L315637] | CD40 RECEPTOR ASSOCIATED FACTOR 1 (CRAF1) (CAP-1), (LMP1 ASSOCIATED PROTEIN) | 12K |
| U45878; [U37546] | INHIBITOR OF APOPTOSIS PROTEIN 1 (HIAP1) (HIAP-1) (C-IAP2) (TNFR2-TRAF SIGNALLING COMPLEX PROTEIN 1) (IAP HOMOLOG C) (IAP1) (MIHC). | 12L |
| U45879; [U37547] | INHIBITOR OF APOPTOSIS PROTEIN 2 (HIAP2) (HIAP-2) (C-IAP1) (TNFR2-TRAF SIGNALLING COMPLEX PROTEIN 2) (IAP HOMOLOG B) (IAP2) (MIHB). | 12M |
| U45880; [U32974] | SIGNALING INHIBITOR OF APOPTOSIS PROTEIN (X-LINKED IAP) (IAP-X-LIKEPROTEIN) (HILP). | 12N |
| | LIGANDS AND RECEPTORS | |
| X01394 | TUMOR NECROSIS FACTOR [TNF-a] | 12O |
| D12614 | LYMPHOTOXIN-ALPHA [FORMERLY TUMOR NECROSIS FACTOR BETA (TNF-b)] | 14B |
| L11015 | LYMPHOTOXIN-BETA | 14C |
| U69611 | TNF-ALPHA CONVERTING ENZYME | 14D |
| D38122; [U08137] | FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL) (APT1LG1) (FASL). | 14E |
| U57059 | APO-2 LIGAND (TNF-RELATED APOPTOSIS INDUCING LIGAND TRAIL) | 14F |

TABLE 4 (CONT)

| GenBank # | Cell Cycle - Gene Name | Array Coordinate |
|----------------------|--|------------------|
| AF017986 | SECRETED APOPTOSIS RELATED PROTEIN 1 | 14G |
| AF017988 | SECRETED APOPTOSIS RELATED PROTEIN 3 (SARP3) | 14H |
| | TUMOR NECROSIS FACTOR RECEPTOR [TUMOR NECROSIS FACTOR RECEPTOR 1 (55KD)] | 15B |
| M33294 | TUMOR NECROSIS FACTOR RECEPTOR [TUMOR NECROSIS FACTOR RECEPTOR 2] | 15C |
| M32315 | FAS/APO 1 | 15D |
| Z70519 | CYTOTOXIC LIGAND TRAIL RECEPTOR | 15E |
| U90875 | DEATH RECEPTOR 5 (DR5) | 15F |
| AF016268 | WSL-LR, WSL-S1, WSL-S2 + TRAMP (Apo-3) (DDR3) | 15G |
| Y09392; [U75380; U74 | INSULIN-LIKE GROWTH FACTOR IA | 15H |
| M27544 | INSULIN-LIKE GROWTH FACTOR II [Somatomedin A] | 16B |
| M29645 | INSULIN-LIKE GROWTH FACTOR I RECEPTOR | 16C |
| X04434 | CATION-INDEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR [insuline-like growth factor receptor II, IGF-2] | 16D |
| Y00285; [J03528] | IGFBP COMPLEX ACID LABILE CHAIN | 16E |
| D25216 | IGFBP2 | 16F |
| M35410 | IGFBP3 (GROWTH HORMONE-DEPENDENT INSULIN-LIKE GROWTH FACTOR-BINDING PROTEIN) | 16G |
| M31159; [M35878] | IGFBP4 | 16H |
| M62403 | IGFBP5 | 17B |
| M65062 | IGFBP6 | 17C |
| M62402 | OTHER REGULATORS | |
| | DEATH-ASSOCIATED PROTEIN 3 (DAP-3) (ionizing radiation resistance conferring protein) | 17D |
| U18321; [X83544] | DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1). | 17E |
| X76104 | Fas-activated serine/threonine kinase (FAST) phosphorylates TIA-1 | 17F |
| X86779 | PDCD2 | 17G |
| S78085 | Akt1 (rac protein kinase alpha, protein kinase B, c-Akt) | 17H |
| M63167 | AKT2 (rac protein kinase beta) | 18B |
| M77198; [M95936] | seven in absentia homolog | 18C |
| U63295 | RATS1 | 18D |
| U37688 | DNA fragmentation factor-45 | 18E |
| U91985 | apoptosis-related protein TFAR15 (TFAR15) | 18F |
| AF022385 | calmodulin dependent phosphodiesterase PDE1B1 | 18G |
| U56976 | | |

TABLE 4 (CONT)

| GenBank # | Cell Cycle - Gene Name | Array Coordinate |
|-----------------|--|------------------|
| U82938 | CD27BP (Siva) | 18H |
| U33286 | chromosome segregation gene homolog CAS | 19B |
| U75285 | apoptosis inhibitor survivin | 19C |
| L25080 | GTP-binding protein (hoA) | 19D |
| L09210 | NITRIC OXIDE SYNTHASE (2A,INDUCIBLE) | 19E |
| M58603 | NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT | 19F |
| M83221 | TRANSCRIPTION FACTOR RELB [L-Rel] | 19G |
| U08015 | NF-ATc [Transcription factor (NFATc.b)] | 20B |
| D15057 | DAD-1 [DEFENDER AGAINST CELL DEATH 1] | 20C |
| | CLUSTERIN [complement lysis inhibitor; testosterone-repressed prostate message 2; apolipoprotein J; sulfated glycoprotein-2] | 20D |
| M74816 | DNA-BINDING PROTEIN INHIBITOR ID-1 | 20E |
| D13889 | GLUTATHIONE REDUCTASE | 20F |
| X15722 | GLUTATHIONE S-TRANSFERASE MICROSOMAL | 20G |
| J03746 | GLUTATHIONE S-TRANSFERASE M4 [GLUTATHIONE S-TRANSFERASE MU 1] | 21B |
| X08020 | GLUTATHIONE S-TRANSFERASE P | 21C |
| X15480 | GLUTATHIONE S-TRANSFERASE A1-1 [Glutathione S-transferase (GST) Ha subunit 1] | 21D |
| M14777 | GLUTATHIONE PEROXIDASE | 21E |
| M21304 | GLUTATHIONE S-TRANSFERASE (THETA 1) | 21F |
| X79389 | NADPH-CYTOCHROME P450 REDUCTASE | 21G |
| S90469 | GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD153 (DNA-DAMAGE INDUCIBLE PROTEIN) (CHOP). | 22B |
| S40706 [S62138] | GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD45 (DNA-DAMAGE INDUCIBLE TRANSCRIPT 1) (DDIT1). | 22C |
| M60974 | DAMAGE INDUCIBLE TRANSCRIPT 1 (DDIT1). | 22D |
| U15172 | NIP1 | 22E |
| U15174 | NIP3 | 22F |
| L07414 | CD40 LIGAND | 22G |
| L08096 | CD27 LIGAND [CD70 antigen] | 23B |
| X96586 | FAN PROTEIN | 23C |
| M84820 | RETINOIC ACID RECEPTOR RXR-BETA | 23D |
| X07282 | RETINOIC ACID RECEPTOR BETA-2 | 23E |
| M93426 | PROTEIN-TYROSINE PHOSPHATASE ZETA | 23F |
| L04791 | EXCISION REPAIR PROTEIN ERCC6 | |

TABLE 4 (CONT)

| GenBank # | Cell Cycle - Gene Name | Array Coordinate |
|-----------|---|---------------------------|
| | UV EXCISION REPAIR PROTEIN RAD23 [xeroderma pigmentosum group | |
| D21090 | C repair complementing protein p58/HHR23B] | 23G |
| | HOUSEKEEPING GENES | |
| | UBIQUITIN | 1A |
| M26880 | | 1B |
| M86400 | PHOSPHOLIPASE A2 | 1C |
| V00530 | HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE | |
| X01677 | GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE | 1D |
| K00558 | TUBULIN ALPHA | 1E |
| M11886 | HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, C-4 ALPHA CHAIN[MHC] | 1F |
| X00351 | BETA-ACTIN | 1G |
| X56932 | 23 kD HIGHLY BASIC PROTEIN | 1H |
| U14971 | RIBOSOMAL PROTEIN S9 | 1I |
| | NEGATIVE CONTROLS | |
| | M13 mp18(+) STRAND DNA | 1J |
| | I-DNA | 1K |
| | pUC 18 | 1L |
| | CALIBRATION MARKERS | 1M1N1O1P |
| | ORIENTATION MARKERS | |
| | Dark spots | 2D2G2J2M3A3P6A6P9A9P12A12 |
| | Faint spots | 2A2B2C2E2F2H2I2K2L2N2O2P4 |
| | Column 13 is blank | |

Human Stress Array

In the human stress array according to the subject invention, all of the unique polynucleotide probe compositions correspond to genes that are associated with stress responses of human cells, e.g. stress response regulators and effectors. In a specific human
5 stress array of interest, the spots are as provided in Table 5.

TABLE 5

| GenBank # | STRESS RESPONSE REGULATORS AND EFFECTORS |
|--------------------------|--|
| K00650 | C-fos |
| M31630 | CAMP RESPONSE ELEMENT BINDING PROTEIN CRE-BP1 (CAMP responsive element binding protein 1) |
| M34356 | CREB (ACTIVE TRANSCRIPTION FACTOR) |
| X60188 | EXTRACELLULAR SIGNAL-REGULATED KINASE 1 (EC 2.7.1.1-) (ERK1) (INSULIN- STIMULATED MAP2 KINASE) (MAP KINASE 1) (MAPK 1) (P44-ERK1) (ERK2) (P44-MAPK) (MICROTUBULE-ASSOCIATED PROTEIN-2 KINASE). |
| M84489 | EXTRACELLULAR SIGNAL-REGULATED KINASE 2 (EC 2.7.1.1-) (ERK2) (MITOGEN- ACTIVATED PROTEIN KINASE 2) (MAP KINASE 2) (MAPK 2) (P42-MAPK) (ERK1). |
| X80692 | EXTRACELLULAR SIGNAL-REGULATED KINASE 3 (EC 2.7.1.1-) (ERK3) (MAP KINASE ISOFORM P97) (P97-MAPK). |
| X59727; S38873 | EXTRACELLULAR SIGNAL-REGULATED KINASE 4 (EC 2.7.1.1-) (ERK4) (MAP KINASE ISOFORM P63) (P63-MAPK). |
| U25278 | EXTRACELLULAR SIGNAL-REGULATED KINASE 5 (EC 2.7.1.1-) (ERK5) (ERK4) (BMK1 KINASE). |
| X79483 | EXTRACELLULAR SIGNAL-REGULATED KINASE 6 (EC 2.7.1.1-) (ERK6) (ERK5). |
| U53442 | MITOGEN-ACTIVATED PROTEIN KINASE P38 BETA (EC 2.7.1.1-) (MAP KINASE P38 BETA). |
| L26318 | STRESS-ACTIVATED PROTEIN KINASE JNK1 (EC 2.7.1.1-) (C-JUN N-TERMINAL KINASE 1) (JNK 46) |
| L31951 | STRESS-ACTIVATED PROTEIN KINASE JNK2 (EC 2.7.1.1-) (C-JUN N-TERMINAL KINASE 2) (JNK 55). |
| U25265; (U71087; U71088) | DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 5 (EC 2.7.1.1-)(MAP KINASE KINASE 5) (MAPKK 5) (MAPK/ERK KINASE 5) (MEK5) |
| | MAP KINASE KINASE MEK5B. |
| | MAP KINASE KINASE MEK5C |

TABLE 5 (CONT)

| GenBank # | STRESS RESPONSE REGULATORS AND EFFECTORS |
|-----------|--|
| U05624 | DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE 1 (EC 2.7.1.-)(MAP KINASE KINASE 1) (MAPK 1) (ERK ACTIVATOR KINASE 1) (MAPK/ERK KINASE) (MEK1). |
| L11285 | DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE 2 (EC 2.7.1.-)(MAP KINASE KINASE 2) (MAPK 2) (ERK ACTIVATOR KINASE 2) (MAPK/ERK KINASE) (MEK2). |
| U39657 | DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE 6 (EC 2.7.1.-)(MAP KINASE KINASE 6) (MAPK 6) (MAPK/ERK KINASE 6) (SAPKK3). |
| U78876 | MEK KINASE 3 |
| D63780 | STE20-LIKE KINASE OXIDANT STRESS KINASE (YSK1, STE20 and SPS1 RELATED KINASE) |
| U77129 | SPS1/STE20 HOMOLOGUE, KHS, ACTIVATOR OF JUN N-TERMINAL KINASE (HSU77129) |
| U07349 | B LYMPHOCYTE GERMINAL CENTER KINASE (HSU07349) |
| U66464 | HEMATOPOIETIC PROGENITOR KINASE ACTIVATOR OF SAPK/JNK (HPK1) (HSU66464) |
| AB005216 | NCK, ASH AND PHOSPHOLIPASE C GAMMA-BINDING PROTEIN NAP4(AB005216) |
| X17576 | NCK MELANOMA CYTOPLASMIC SRC HOMOLOGUE (HSNCK) |
| U24153 | SERINE/THREONINE-PROTEIN KINASE PAK-GAMMA (EC 2.7.1.-) (GAMMA-PAK) (P21-ACTIVATED KINASE 3) (PAK65) (S6/H4 KINASE) (PAK2) PAK3. |
| M35543 | G25K GTP-BINDING PROTEIN, BRAIN ISOFORM (GP) (CDC42 HOMOLOG) CDC42. |
| U12595 | TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN(TRAP1)(HSU12595) |
| U12596 | TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN(TRAP2) (HSU12596) |
| X17620 | NUCLEOSIDE DIPHOSPHATE KINASE A (EC 2.7.4.6) (NDK A) (NDP KINASE A) (TUMOR METASTATIC PROCESS-ASSOCIATED PROTEIN) (METASTASIS INHIBITION FACTOR NM23) (NM23-H1). |
| M64673 | HEAT SHOCK FACTOR PROTEIN 1 (HSF 1) (HEAT SHOCK TRANSCRIPTION FACTOR 1)(HSIF 1). |
| M65217 | HEAT SHOCK FACTOR PROTEIN 2 (HSF 2) (HEAT SHOCK TRANSCRIPTION FACTOR 2)(HSIF 2). |
| D87673 | HEAT SHOCK TRANSCRIPTION FACTOR 4. |
| L34075 | FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) (HUMFRAPX) |

TABLE 5 (CONT)

| GenBank # | STRESS RESPONSE REGULATORS AND EFFECTORS |
|--|--|
| M35663; (U50648) | INTERFERON-INDUCIBLE RNA-DEPENDENT PROTEIN KINASE (P68 KINASE) |
| U07550 | 10 KD HEAT SHOCK PROTEIN, MITOCHONDRIAL (HSP10) (10 KD CHAPERONIN) (CPN10). |
| D86956 | HEAT-SHOCK PROTEIN 110 KD (KIAA0201) |
| X54079; X03900; L39370; X16477; Z23090; S74571) | HEAT SHOCK 27 KD PROTEIN (HSP 27)(STRESS-RESPONSIVE PROTEIN 27)(SRP27)(ESTROGEN-REGULATED 24 KD PROTEIN) (28 KD HEAT SHOCK PROTEIN). |
| X61598; D83174 | 47 KD HEAT SHOCK PROTEIN PRECURSOR (COLLAGEN-BINDING PROTEIN 1) (COLLIGIN 1) |
| | Collagen binding protein 2 (HUMCBP2). |
| M11717; (M59828) | HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2). |
| L26336 | HEAT SHOCK-RELATED 70 KD PROTEIN 2 (HEAT SHOCK 70 KD PROTEIN 2). |
| L12723 | HEAT SHOCK 70 KD PROTEIN 4 (HSP70RY). |
| X51757; M11236 | HEAT SHOCK 70 KD PROTEIN 6 (HEAT SHOCK 70 KD PROTEIN B). |
| | HEAT SHOCK 70 KD PROTEIN 7 (HEAT SHOCK 70 KD PROTEIN B) (FRAGMENT). |
| Y00371 | HEAT SHOCK COGNATE 71 KD PROTEIN. |
| X07270; (X15183; M27024; M30626; M30627) | HEAT SHOCK PROTEIN HSP 90-ALPHA (HSP 86). |
| M16660 | HEAT SHOCK PROTEIN HSP 90-BETA (HSP 84) (HSP 90) |
| U15590 | HEAT SHOCK PROTEIN 27 (heart) |
| S67070 | HEAT SHOCK PROTEIN HSP72 HOMOLOG (FRAGMENT). |
| U40992 | HEAT SHOCK PROTEIN HSP40HEAT SHOCK PROTEIN HSP40 HOMOLOG. |
| L15189 | REGULATED PROTEIN) (GRP 75) (PEPTIDE-BINDING PROTEIN 74) (PBP74) (MORTALIN) (MOT). |
| U28918 | HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN) |
| D13388 | DNAJ PROTEIN HOMOLOG 2 (DNAJ2 OR HDJ2) |
| D49547; (D17749; D85429) | HEAT SHOCK PROTEIN 40 |
| M19645 | 78 KD GLUCOSE REGULATED PROTEIN PRECURSOR (GRP 78) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN) (BIP). |

TABLE 5 (CONT)

| GenBank # | STRESS RESPONSE REGULATORS AND EFFECTORS |
|---|--|
| L10284; (L18887; M94859; M98452) | CALNEXIN PRECURSOR (MAJOR HISTOCOMPATIBILITY COMPLEX CLASS I ANTIGEN-BINDING PROTEIN P88) (P90) (IP90) |
| M84739 | CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60)(52 KD RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A) |
| J05016 | PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72) |
| L24804; (L24805) | P23 PROGESTERONE RECEPTOR ASSOCIATED PROTEIN (HUMPR4) |
| M86752 | TRANSFORMATION - SENSITIVE PROTEIN (IEF SSP 3521) |
| L11667 | CYCLOPHILIN-40 |
| U73704 | 48 kDa FKBP-ASSOCIATED PROTEIN FAP48 |
| U42031 | 54 KDA PROGESTERONE RECEPTOR-ASSOCIATED PROTEIN FKBP54 |
| M34539; (M80199; M80706; M92423; J05340; X55741; X52220) | FK506-BINDING PROTEIN (FKBP) (FKBP12) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (ROTAMASE) |
| M88279 | IMMUNOPHILIN (FKBP52) |
| M65128 | RAPAMYCIN-BINDING PROTEIN (FKBP-13) |
| X56134 (M14144; Z19554) | VIMENTIN, INTERMEDIATE FILAMENT PROTEIN |
| M34664; (M22382) | MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (P60 LYMPHOCYTE PROTEIN) (HSPD1 OR HSP60) (CHAPERONIN HOMOLOG) (HUCHA60) (HEAT SHOCK PROTEIN 60) |
| S83171; (Z35491) | BCL-2 BINDING ATHANOGENE-1 (BAG-1) (GLUCOCORTICOID RECEPTOR-ASSOCIATED PROTEIN RAP46) |
| D23662 | UBIQUITIN-LIKE PROTEIN (NEDD8) |
| X52882 | T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)(CCT-ALPHA) CCT1 OR CCTA OR TCP1 |
| U38846 | T-COMPLEX PROTEIN 1, DELTA SUBUNIT (TCP-1-DELTA)(CCT-DELTA) (STIMULATOR OF TAR RNA BINDING) (HSU38846). |
| D43950 | T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON)(CCT-EPSILON) (HUMKG1DD) |
| X74801; (U17104) | T-COMPLEX PROTEIN 1, GAMMA SUBUNIT (TCP-1-GAMMA)(CCT-GAMMA) (CCT3) OR (CCTG) OR (TRIC5) (HSHUMAPC). |

TABLE 5 (CONT)

| GenBank # | STRESS RESPONSE REGULATORS AND EFFECTORS |
|----------------------------------|--|
| U83843 | T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA)(HIV-1 NEF INTERACTING PROTEIN) (HSU83843). |
| D13627 | T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA)(CCT-THETA) (HUMRSC548). |
| X06985 | HEME OXYGENASE 1 (EC 1.14.99.3) (HO-1) (HSOXYGR). |
| D21243; (S34389) | HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2) |
| X15187; (M33716) | ENDOPLASMIN PRECURSOR (94 KD GLUCOSE-REGULATED PROTEIN)(GRP94) (GP96 HOMOLOG) (TUMOR REJECTION ANTIGEN 1) (HSTRA1). |
| U05569 | ALPHA CRYSTALLIN A CHAIN (HSU05569). |
| S45630 | ALPHA CRYSTALLIN B CHAIN (ALPHA(B)-CRYSTALLIN) (ROSENTHAL FIBER COMPONENT). |
| U59058 | BETA CRYSTALLIN A3 (HSU59058). |
| U59057 | BETA CRYSTALLIN A4 (HSU59057). |
| U35340 | BETA CRYSTALLIN B1 (CRYBB1) (HSU35340). |
| L10035 | BETA CRYSTALLIN B2 (BP) (HUMCRYB2B). |
| U71216 | BETA CRYSTALLIN B3 (9CRYBB3 OR CRYB3) (HSU71216). |
| L38869 | BETA CRYSTALLIN S (GAMMA CRYSTALLIN S) (CRYGS) OR (GRYG8). |
| U66582; M11971; (M11970) | GAMMA CRYSTALLIN C (GAMMA CRYSTALLIN 2 OR 1/3) (CRYGC) OR (CRYG3). |
| L02950 | GAMMA CRYSTALLIN B (GAMMA CRYSTALLIN 1-2) (CRYGB) OR (CRYG2) (HUMCRYGX1). |
| L13278; (S58039) | MU-CRYSTALLIN HOMOLOG (CRYM) (HUMMUCRY). |
| D16234; (Z49835; D83485; U42068) | QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN). |
| D49489 | PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (EC 5.3.4.1) (ERP60) (58KDA MICROSOMAL PROTEIN) (phospholipase C-alpha) |
| M75715 | PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1) (HUMP5). |
| | EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1) (TB3-1) (C11 PROTEIN) RF1. |
| D49490 | PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (EC 5.3.4.1) (PDIR) (HUMPDIR). |
| J02783; (X05130; X07077) | PROTEIN DISULFIDE ISOMERASE PRECURSOR (PD) (EC 5.3.4.1) / PROLYL 4-HYDROXYLASE BETA SUBUNIT (EC 1.14.11.2) / CELLULAR THYROID HORMONE BINDING PROTEIN (P55)(HSPRO4HY). |

TABLE 5 (CONT)

| GenBank # | STRESS RESPONSE REGULATORS AND EFFECTORS |
|---------------------------|--|
| | Glutathione-insulin transhydrogenase (EC 5.3.4.1 / 1.8.4.2); protein-disulfide reductase (glutathione) (HSGIIR). |
| M86737 | STRUCTURE-SPECIFIC RECOGNITION PROTEIN 1 (SSRP1) (RECOMBINATION SIGNAL SEQUENCE RECOGNITION PROTEIN) (T160) SSRP1. |
| X63368; (S37374; S37375) | DNAJ PROTEIN HOMOLOGS HSJ1A protein; HSJ1B protein. (HSJ-1)(HSJ1MR) |
| U65785 | 150 KDA OXYGEN-REGULATED PROTEIN ORP150 (HSU65785) |
| X90392 : (L40817; U06846) | DNA DAMAGE RESPONSE/REPAIR/RECOMBINATION |
| L24564 | MUSCLE-SPECIFIC DNASE I-LIKE (DNase X) (XIB) |
| M96684 | RAD |
| M29971 | TRANSCRIPTIONAL ACTIVATOR PROTEIN PUR-ALPHA |
| U09579; (L25610) | METHYLATED-DNA--PROTEIN-CYSTEINE METHYLTRANSFERASE (6-O-METHYLGUANINE-DNA METHYLTRANSFERASE) (MGMT) |
| L37374 | CYCLIN-DEPENDENT KINASE INHIBITOR 1 (MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN 6) (MDA-6) (P21) (CDK-INTERACTING PROTEIN 1) (CIP1) (WAF1) (CDKN1A) (CDKN1) (SDI1) (PIC1) (CAP20) |
| U70310 | FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) (FEN-1) |
| HT3218 (X02317; K00065) | DNA REPAIR PROTEIN XRCC9 |
| J02947 | SUPEROXIDE DISMUTASE (CU-ZN) (EC 1.15.1.1) SOD1. |
| X07834; (X59445) | EXTRACELLULAR SUPEROXIDE DISMUTASE PRECURSOR (CU-ZN) (EC 1.15.1.1) (EC-SOD) SOD3. |
| M14694; (M14695) | SUPEROXIDE DISMUTASE PRECURSOR (MN) (EC 1.15.1.1) SOD2 |
| Z12020; (M92424) | CELLULAR TUMOR ANTIGEN P53 |
| | MDM2 PROTEIN (P53-ASSOCIATED PROTEIN) |
| | MDM2-A (GB: U33199) |
| | MDM2-C (GB: U33201) |
| U33841 | ATAXIA TELANGIECTASIA (ATM) |
| J03250 | DNA TOPOISOMERASE I (TOPI) |
| J04088 | DNA TOPOISOMERASE II, ALPHA (TOP2A) |
| X68060 | DNA TOPOISOMERASE II, BETA (TOP2B) |
| U43431 | DNA TOPOISOMERASE III (TOP3) |

TABLE 5 (CONT)

| GenBank # | STRESS RESPONSE REGULATORS AND EFFECTORS |
|------------------|---|
| S40706 (S62138) | GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD153 (DNA-DAMAGE INDUCIBLE TRANSCRIPT 3) (DDIT3) (C/EBP-HOMOLOGOUS PROTEIN) (CHOP) |
| X04076 | CATALASE (EC 1.11.1.6) CAT. |
| X51420 | 5,6-DIHYDROXYINDOLE-2-CARBOXYLIC ACID OXIDASE PRECURSOR (DHICA OXIDASE) (TYROSINASE-RELATED PROTEIN 1) (TRP-1) (CATALASE B) (GLYCOPROTEIN-75) (GP75) |
| | BASE EXCISION REPAIR |
| X15653 | URACIL-DNA GLYCOSYLASE PRECURSOR (UNG1) |
| X52486 | URACIL-DNA GLYCOSYLASE 2 (UNG2) |
| M74905 | DNA-3 METHYLADENINE GLYCOSYLASE (3-METHYLADENINE DNA GLYCOSYLASE) (ADPG) (3-ALKYLADENINE DNA GLYCOSYLASE) (N-METHYLPURINE-DNA GLYCOSIRASE) (MPG) (MAG1) (3MeAG) |
| U51166 | G/T MISMATCH-SPECIFIC THYMINE DNA GLYCOSYLASE (TDG) |
| Y11838 | 8-OXYGUANINE DNA GLYCOSYLASE HOMOLOG 1 (mutM HOMOLOG) (OGH1) (HOGG1) (FaPyG) |
| U63329 | mutY HOMOLOG (HMYH) |
| X59764; (X66133) | DNA-(APURINIC OR APYRIMIDINIC SITE) LYASE (AP ENDONUCLEASE 1) (APEX NUCLEASE) (APEN) (REF-1 PROTEIN) (APE1) |
| U79718 | ENDONUCLEASE III HOMOLOG 1 (HNTH1) (OCIS3) |
| M36067 | DNA LIGASE I (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP)) (DNL1) (LIG1) |
| X84740 | DNA LIGASE III (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP)) (DNL3) |
| M18112 | POLY (ADP-RIBOSE) POLYMERASE (PARP) (ADPRT) (NAD (+) ADP-RIBOSYLTRANSFERASE) (POLY (ADP-RIBOSE) SYNTHETASE) (PPOL) |
| D16581 | 7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (mutT HOMOMOLOG) (8-OXO-DGTPASE) (MTH1) |
| M36089 | DNA-REPAIR PROTEIN XRCC1 |
| D29013 | DNA POLYMERASE BETA (DPOB) |
| M11722 | DNA NUCLEOTIDYLEXOTRANSFERASE (TERMINAL ADDITION ENZYME) (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFERASE) (DNIT) (TDI) |
| X55715 | 40S RIBOSOMAL PROTEIN S3 (POSSIBLE drpase) |
| | NUCLEOTIDE EXCISION REPAIR |

TABLE 5 (CONT)

| STRESS RESPONSE REGULATORS AND EFFECTORS | |
|--|---|
| D14533 | DNA-REPAIR PROTEIN COMPLEMENTING XP-A CELLS (XERODERMA PIGMENTOSUM GROUP A COMPLEMENTING PROTEIN) |
| M31899 | DNA-REPAIR PROTEIN COMPLEMENTING XP-B CELLS (XERODERMA PIGMENTOSUM GROUP B COMPLEMENTING PROTEIN) (DNA EXCISION REPAIR PROTEIN ERCC3) (BASAL TRANSCRIPTION FACTOR 2 89 KD SUBUNIT) (BTF2-p89) (TFIIH 89 KD SUBUNIT) |
| D21089 | DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS (XERODERMA PIGMENTOSUM GROUP C COMPLEMENTING PROTEIN) (p125) |
| D21235 | UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A) |
| D21090 | UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG B (HHR23B) (XP-C REPAIR COMPLEMENTING COMPLEX 58 KD PROTEIN) (p58) |
| X52221: (H11175) | DNA-REPAIR PROTEIN COMPLEMENTING XP-D CELLS (XERODERMA PIGMENTOSUM GROUP D COMPLEMENTING PROTEIN) (DNA EXCISION REPAIR PROTEIN ERCC-2) |
| U18299 | DAMAGE-SPECIFIC DNA BINDING PROTEIN p127 SUBUNIT; IMPLICATED IN XERODERMA PIGMENTOSUM GROUP E (DDB1) |
| U18300 | DAMAGE-SPECIFIC DNA BINDING PROTEIN p48 SUBUNIT; IMPLICATED IN XERODERMA PIGMENTOSUM GROUP E (DDB2) |
| L77890 | DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELLS (XERODERMA PIGMENTOSUM GROUP F COMPLEMENTING PROTEIN) (DNA EXCISION REPAIR PROTEIN ERCC-4) |
| L20046: (X69978) | DNA-REPAIR PROTEIN COMPLEMENTING XP-G CELLS (XERODERMA PIGMENTOSUM GROUP G COMPLEMENTING PROTEIN) (DNA EXCISION REPAIR PROTEIN ERCC-5) |
| U28413 | COCKayne SYNDROME GROUP A: WD-REPEAT PROTEIN (CSA PROTEIN) |
| I04791 | EXCISION REPAIR PROTEIN ERCC-6 (CSB) |
| M95809 | BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (p62) (BTF2p62) |
| Z30094 | BASIC TRANSCRIPTION FACTOR 2, 44 KD SUBUNIT (BTF2p44) |
| Z30093 | BASIC TRANSCRIPTION FACTOR 2, 34 KD SUBUNIT (BTF2p34) |
| Y07595 | BASIC TRANSCRIPTION FACTOR 2, 52 KD SUBUNIT (BTF2p52) |
| M13194 | DNA EXCISION REPAIR PROTEIN ERCC-1 |

TABLE 5 (CONT)

| GenBank # | STRESS RESPONSE REGULATORS AND EFFECTORS |
|-----------------|--|
| M63488 | REPLICATION PROTEIN A 70 KD DNA-BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE STRANDED DNA-BINDING PROTEIN) |
| J05249 | REPLICATION PROTEIN A 32 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 2) |
| L07493 | REPLICATION PROTEIN A 14 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR A PROTEIN 3) |
| U24186 | REPLICATION PROTEIN A 30 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 4) |
| M15796; J04718 | PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA) (CYCLIN) |
| L07540 | ACTIVATOR 1 36 KD SUBUNIT (REPLICATION FACTOR C 36 KD SUBUNIT) (RFC36) |
| M87339 | ACTIVATOR 1 37 KD SUBUNIT (REPLICATION FACTOR C 37 KD SUBUNIT) (RFC37) |
| L07541 | ACTIVATOR 1 38 KD SUBUNIT (REPLICATION FACTOR C 38 KD SUBUNIT) (RFC38) |
| M87338 | ACTIVATOR 1 40 KD SUBUNIT (REPLICATION FACTOR C 40 KD SUBUNIT) (RFC40) |
| L14922 | ACTIVATOR 1 140KD SUBUNIT (REPLICATION FACTOR C LARGE SUBUNIT) (A1 140 KD SUBUNIT) (RF-C 140 KD SUBUNIT) (ACTIVATOR 1 LARGE SUBUNIT) (DNA-BINDING PROTEIN PO-GA) |
| X06745 | DNA POLYMERASE ALPHA |
| M80397 | DNA POLYMERASE DELTA CATALYTIC CHAIN |
| M60974 | GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD-45 (DNA-DAMAGE INDUCIBLE TRANSCRIPT 1) (DDIT1) (GA45) |
| S40706 (S62138) | GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD153 (DNA-DAMAGE INDUCIBLE PROTEIN) (CHOP) |
| | Homologous recombination |
| U63139 | DNA REPAIR PROTEIN RAD50 |
| D13804; D14134 | DNA REPAIR PROTEIN RAD51 HOMOLOG |
| U12134 | DNA REPAIR PROTEIN RAD52 HOMOLOG |
| U09820 | X-LINKED HELICASE II (X-LINKED NUCLEAR PROTEIN) (XNP) (RAD54L) (XH2) |
| X97795 | DNA REPAIR PROTEIN RAD54 HOMOLOG |
| U14680 | BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN (BRCA1) |
| U43746 | BREAST CANCER TYPE 2 SUSCEPTIBILITY PROTEIN (BRCA2) |
| D63882 | MEIOTIC RECOMBINATION PROTEIN DMC1/UM15 HOMOLOG |
| X83441 | DNA LIGASE IV (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP)) (DNL4) |

TABLE 5 (CONT)

| GenBank # | STRESS RESPONSE REGULATORS AND EFFECTORS |
|-------------------|--|
| M74524 | HHR6A (YEAST RAD6 HOMOLOG) (UBIQUITIN-CONJUGATING ENZYME) (UBCA) |
| M74525 | HHR6B (YEAST RAD6 HOMOLOG) (UBIQUITIN-CONJUGATING ENZYME) (UBCB) |
| Y08837 | RAD51-LIKE PROTEIN (POSSIBLE XRCC2) |
| | Non-homologous end-rejoining |
| U40622 | DNA REPAIR PROTEIN XRCC4 |
| M32865 : (S38729) | ATP-DEPENDENT DNA HELICASE II, 70 KD SUBUNIT (LUPUS KU AUTOANTIGEN PROTEIN P70) (70 KD SUBUNIT OF KU ANTIGEN) (THYROID-LUPUS AUTO-ANTIGEN) (TLAA) (KU70) (CTC BOX BINDING FACTOR 75 KD SUBUNIT) (CTCBF) (CTC75) (XRCC6) |
| M30938 | ATP-DEPENDENT DNA HELICASE II, 86 KD SUBUNIT (LUPUS KU AUTOANTIGEN PROTEIN P86) (86 KD SUBUNIT OF KU ANTIGEN) (THYROID-LUPUS AUTOANTIGEN) (TLAA) (CTC BOX BINDING FACTOR 85 KD SUBUNIT) (CTCBF) (CTC85) (NUCLEAR FACTOR IV) (KU80) (XRCC5) |
| U35835: (U47077) | DNA-DEPENDENT PROTEIN KINASE (DNA-PK) |
| | DNA DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT (DNA-PKcs) (XRCC7) |
| M29474 | V(D)J RECOMBINATION ACTIVATING PROTEIN 1 (RAG-1) |
| M94633 | V(D)J RECOMBINATION ACTIVATING PROTEIN 2 (RAG-2) |
| | MISMATCH REPAIR |
| U07418: (U07343) | DNA MISMATCH REPAIR PROTEIN MLH1 (mutL HOMOLOG) |
| U04045: (L47583) | DNA MISMATCH REPAIR PROTEIN MSH2 |
| J04810 | DNA MISMATCH REPAIR PROTEIN MSH3 (DIVERGENT UPSTREAM PROTEIN) (MISMATCH REPAIR PROTEIN 1) (MRP1) (DUP) (DUG) |
| U54777 | DNA MISMATCH REPAIR PROTEIN MSH6 (muIs - ALPHA 160 KD SUBUNIT) (G/T MISMATCH BINDING PROTEIN) (GTBP) (GTMBP) (P160) |
| U13696 | DNA MISMATCH REPAIR PROTEIN PMS2 (PMS1 PROTEIN HOMOLOG 2) |
| U13695 | DNA MISMATCH REPAIR PROTEIN PMS1 (PMS1 PROTEIN HOMOLOG 1) |
| | DRUG/XENOBIOTIC METABOLISM |
| X14672: X17059 | ARYLAMINE N-ACETYLTRANSFERASE, POLYMORPHIC (EC 2.3.1.5) (PNAT) + |
| | ARYLAMINE N-ACETYLTRANSFERASE, MONOMORPHIC (EC 2.3.1.5) (MNAT) |
| Z00036 | CYTOCHROME P450 IA2 (EC 1.14.14.1) (P450-P3) (P450-4) 515 |
| Z00036 | CYTOCHROME P450 IA2 (EC 1.14.14.1) (P450-P3) (P450-4) 515 |

TABLE 5 (CONT)

| GenBank # | STRESS RESPONSE REGULATORS AND EFFECTORS |
|---|---|
| J04449; D00003; J04813; D00408 | CYTOCHROME P450 IIIA4 (EC 1.14.14.1) (NIFEDIPINE OXIDASE) (NF-25) (P450-PCN1) |
| | CYTOCHROME P450 IIIA3 (EC 1.14.14.1) (GLUCOCORTICOID-INDUCIBLE) (HLP) CYP3A3. |
| | CYTOCHROME P450 IIIA5 (EC 1.14.14.1) (P450-PCN3) |
| | CYTOCHROME P450 IIIA7 (EC 1.14.14.1) (P450-HFLA) |
| J02871 | CYTOCHROME P450 IVB1 (EC 1.14.14.1) (P450-HP) |
| M33318; X13930; X13897; M33317 | CYTOCHROME P450 IIA6 (EC 1.14.14.1) (COUMARIN 7-HYDROXYLASE) (IIA3) (P450Q1) (PHENOBARBITAL-INDUCIBLE) |
| | CYTOCHROME P450 IIA7 (EC 1.14.14.1) (P450-IIA4) |
| | CYTOCHROME P450 IIC9 (EC 1.14.14.1) (P450 PB-1) (P450 MP-4) (S-MEPHENYTOIN 4-HYDROXYLASE) |
| M21940; M15331; (M21939)M61858; (L07093); M61853; M61854 | CYTOCHROME P450 II |
| U09178 | DIHYDROPYRIMIDINE DEHYDROGENASE (NADP+) PRECURSOR (EC 1.3.1.2) (DPD) (DIHYDROURACIL DEHYDROGENASE) (DIHYDROTHYMINE DEHYDROGENASE) DPYD. |
| M64082 | DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 1 (EC 1.14.13.8) (FETAL HEPATIC FLAVIN-CONTAINING MONOOXYGENASE 1) (FMO 1) (DIMETHYLANILINE OXIDASE 1) |
| M83772 | DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 3 (EC 1.14.13.8) (HEPATIC FLAVIN-CONTAINING MONOOXYGENASE 3) (FMO 3) (DIMETHYLANILINE OXIDASE 3) (FMO II) |
| Z11737 | DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 4 (EC 1.14.13.8) (HEPATIC FLAVIN-CONTAINING MONOOXYGENASE 4) (FMO 4) (DIMETHYLANILINE OXIDASE 4) |
| L37080 | DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 5 (EC 1.14.13.8) (HEPATIC FLAVIN-CONTAINING MONOOXYGENASE 5) (FMO 5) (DIMETHYLANILINE OXIDASE 5) |

TABLE 5 (CONT)

| GenBank # | STRESS RESPONSE REGULATORS AND EFFECTORS |
|--|---|
| GenBank # | STRESS RESPONSE REGULATORS AND EFFECTORS |
| X04808 | PORPHOBILIN DEAMINASE (EC 4.3.1.8) (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN SYNTHASE) |
| M14758 | MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1) |
| M23234 | MULTIDRUG RESISTANCE PROTEIN 3 (P-GLYCOPROTEIN 3) |
| U05628 | MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 1 |
| U08021 | NICOTINAMIDE N-METHYLTRANSFERASE (EC 2.1.1.1) |
| U09031; U28170; L19956 | PHENOL-SULFATING PHENOL SULFOTRANSFERASE 1 (EC 2.8.2.1) (P-PST) (THERMOSTABLE PHENOL SULFOTRANSFERASE) (TS-PST) (HAST1/HAST2) (ST1A3) STP1 OR STP. |
| | PHENOL-SULFATING PHENOL SULFOTRANSFERASE 2 (EC 2.8.2.1) (P-PST) (ST1A2) STP2. |
| | MONOAMINE-SULFATING PHENOL SULFOTRANSFERASE (EC 2.8.2.1) (SULFOTRANSFERASE MONOAMINE-PREFERRING) (M-PST) (THERMOLABILE PHENOL SULFOTRANSFERASE) (TL-PST) (PLACENTAL ESTROGEN SULFOTRANSFERASE) (CATECHOLAMINE-SULFATING PHENOL SULFOTRANSFERASE) (HAST3) STM. |
| U08854; X63359; U06641; J05428; Y00317 | UDP-GLUCURONOSYLTRANSFERASE 2B15 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPGT) (UDPGTH-3) UGT2B15. |
| | UDP-GLUCURONOSYLTRANSFERASE 2B10 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPGT) UGT2B10. |
| | UDP-GLUCURONOSYLTRANSFERASE 2B8 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPGT) (ESTRIOL SPECIFIC) (HLUG4) (FRAGMENT) UGT2B8. |
| | UDP-GLUCURONOSYLTRANSFERASE 2B7 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPGT) (3,4-CATECHOL ESTROGEN SPECIFIC) (UDPGTH-2) UGT2B7. |
| | UDP-GLUCURONOSYLTRANSFERASE 2B4 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPGT) (HYDROXYCHOLIC ACID) (HLUG25) (UDPGTH-1) UGT2B4. |

TABLE 5 (CONT)

| GenBank # | STRESS RESPONSE REGULATORS AND EFFECTORS |
|------------------|---|
| M68840 | AMINE OXIDASE (FLAVIN-CONTAINING) A (EC 1.4.3.4) (MONOAMINE OXIDASE) (MAO-A) MAOA. |
| M69177 | AMINE OXIDASE (FLAVIN-CONTAINING) B (EC 1.4.3.4) (MONOAMINE OXIDASE) (MAO-B) MAOB. |
| K03191 | CYTOCHROME P450 1A1 (EC 1.14.14.1) (P450-P1) (P450 FORM 6) (P450-C) (TCDD-INDUCIBLE). |
| M29874 | CYTOCHROME P450 1B6 (EC 1.14.14.1) (PHENOBARBITAL-INDUCIBLE) (P450 1B1). |
| M20403 | CYTOCHROME P450 1B6 (EC 1.14.14.1) (P450-DB1) (DEBRISOQUINE 4-HYDROXYLASE) CYP2D6. |
| J02625 | CYTOCHROME P450 1E1 (EC 1.14.14.1) (P450-J) (ETHANOL INDUCIBLE) CYP2E1 |
| J02906 | CYTOCHROME P450 1F1 (EC 1.14.14.1) CYP2F1. |
| M14565 | CYTOCHROME P450 XIA1, MITOCHONDRIAL PRECURSOR (EC 1.14.15.6) (P450(SCC)) (CHOLESTEROL SIDE-CHAIN CLEAVAGE ENZYME) (CHOLESTEROL DESMOLASE) CYP11A1. |
| X55764 | CYTOCHROME P450 XI1 PRECURSOR (P450C11) (STEROID 11-BETA-HYDROXYLASE) (EC 1.14.15.4) CYP11B1 OR S11B1. |
| M12792: (M23280) | CYTOCHROME P450 XXIB (EC 1.14.99.10) (STEROID 21-HYDROXYLASE) (P450-C21B) CYP21B OR CYP21 OR CYP21A2. |
| I07765 | LIVER CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ACYL COENZYME A:CHOLESTEROL ACYLTRANSFERASE) (ACAT) (MONOCYTE/MACROPHAGE SERINE ESTERASE) (HMSE) CES2. |
| J05459 | GLUTATHIONE S-TRANSFERASE MU 3 (EC 2.5.1.18) (GSTM3-3) (CLASS-MU) GSTM3 OR GST5. |
| D13889 | GLUTATHIONE REDUCTASE |
| X15722 | GLUTATHIONE S-TRANSFERASE MICROSOMAL |
| J03746 | GLUTATHIONE S-TRANSFERASE M4 (GLUTATHIONE S-TRANSFERASE MU 1) |
| X08020 | GLUTATHIONE S-TRANSFERASE P |
| X15480 | GLUTATHIONE S-TRANSFERASE A1-1 (Glutathione S-transferase (GST) Ha subunit 1) |
| M14777 | GLUTATHIONE PEROXIDASE |
| M21304 | GLUTATHIONE S-TRANSFERASE (THETA 1) |
| AF010316 | GLUTATHIONE S-TRANSFERASE HOMOLOG |
| I05779 | SOLUBLE EPOXIDE HYDROLASE (SEH) (EC 3.3.2.3) (EPOXIDE HYDRATASE) (CYTOSOLIC EPOXIDE HYDROLASE) (CEH) EPHX2. |

TABLE 5 (CONT)

| GenBank # | STRESS RESPONSE REGULATORS AND EFFECTORS |
|-----------|--|
| M57899 | UDP-GLUCURONOSYLTRANSFERASE 1-1 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPGT) (UGT-1A) (UGT1*1) (UGT1-01) (UGT1.1) (UGT1A1) (BILIRUBIN SPECIFIC ISOZYME 1) (UGT1A) (HUG-BR1) UGT1 OR GNT1. |
| S55985 | UDP-GLUCURONOSYLTRANSFERASE 1-2 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPGT) (UGT-1B) (UGT1*2) (UGT1-02) (UGT1.2) (UGT1A2) (UGT1B) (HUGP4) UGT1 OR GNT1. |
| M84127 | UDP-GLUCURONOSYLTRANSFERASE 1-3 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPGT) (UGT-1C) (UGT1*3) (UGT1-03) (UGT1.3) (UGT1A3) (UGT1C) UGT1 OR GNT1. |
| M57951 | UDP-GLUCURONOSYLTRANSFERASE 1-4 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPGT) (UGT-1D) (UGT1*4) (UGT1-04) (UGT1.4) (UGT1A4) (UGT1D) (BILIRUBIN SPECIFIC ISOZYME 2) (HUG-BR2) UGT1 OR GNT1. |
| J04093 | UDP-GLUCURONOSYLTRANSFERASE 1-6 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPGT) (UGT-1F) (UGT1*6) (UGT1-06) (UGT1.6) (UGT1A6) (UGT1F) (PHENOL SPECIFIC) UGT1 OR GNT1. |
| X71480 | CYTOCHROME P450 IVA11 (EC 1.14.14.1) (FRAGMENT) CYP4A-11. |
| X83573 | ARYLSULFATASE E PRECURSOR (EC 3.1.6.-) (ASE) ARSE. |
| X92106 | BLEOMYCIN HYDROLASE (EC 3.4.22.-) (BLM HYDROLASE). |
| M65212 | CATECHOL O-METHYLTRANSFERASE, MEMBRANE-BOUND FORM (EC 2.1.1.6) (MB-COMT) (CONTAINS: CATECHOL O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)) COMT. |
| Z28409 | COPROPORPHYRINOGEN III OXIDASE PRECURSOR (EC 1.3.3.3) (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE) (COX) CPO. |
| Y09501 | NADH-CYTOCHROME B5 REDUCTASE (EC 1.6.2.2) (B5R) DIA1. |
| U12778 | ACYL-COA DEHYDROGENASE, SHORT/Branched CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2-METHYL BRANCHED CHAIN ACYL-COA DEHYDROGENASE) (2-MEBCAD) ACADS8. |
| M74542 | ALDEHYDE DEHYDROGENASE, DIMERIC NADP-PREFERRING (EC 1.2.1.5) (CLASS 3) ALDH3. |

TABLE 5 (CONT)

| GenBank # | STRESS RESPONSE REGULATORS AND EFFECTORS |
|-----------|---|
| X53463 | GLUTATHIONE PEROXIDASE-GASTROINTESTINAL (EC 1.11.1.9) (GSHPX-GI) (GLUTATHIONE PEROXIDASE-RELATED PROTEIN 2) (GPRP) GPX2. |
| X71973 | PHOSPHOLIPID HYDROPEROXIDE GLUTATHIONE PEROXIDASE (EC 1.11.1.9) (PHGPX) GPX4. |
| M63012 | SERUM PEROXONASE/ARYLESTERASE 1 (EC 3.1.1.2) (EC 3.1.8.1) (PON 1) (SERUM ARYLDIARYLPHOSPHATASE 1) (A-ESTERASE 1) (AROMATIC ESTERASE 1) PON1 OR PON. |
| L48513 | SERUM PEROXONASE/ARYLESTERASE 2 (EC 3.1.1.2) (EC 3.1.8.1) (PON 2) (SERUM ARYLDIARYLPHOSPHATASE 2) (A-ESTERASE 2) (AROMATIC ESTERASE 2) PON2. |
| L48516 | SERUM PEROXONASE/ARYLESTERASE 3 (EC 3.1.1.2) (EC 3.1.8.1) (PON 3) (SERUM ARYLDIARYLPHOSPHATASE 3) (A-ESTERASE 3) (AROMATIC ESTERASE 3) (FRAGMENT) PON3. |
| S62904 | THIOPURINE S-METHYLTRANSFERASE (EC 2.1.1.67) (THIOPURINE METHYLTRANSFERASE) TPMT. |
| L02932 | PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA) PPARA OR PPAR |
| L07592 | PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR BETA (PPAR-BETA) (PPAR-DELTA) (NUCLEAR HORMONE RECEPTOR 1) (NUC1) (NUC1) PPARB OR PPARD. |
| | HOUSEKEEPING GENES |
| M26880 | UBIQUITIN |
| M86400 | PHOSPHOLIPASE A2 |
| V00530 | HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE |
| X01677 | GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE |
| K00558 | TUBULIN ALPHA |
| M11886 | HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, C-4 ALPHA CHAIN |
| [MHC] | 902 |
| X00351 | BETA-ACTIN |
| X56932 | 23 kD HIGHLY BASIC PROTEIN |
| U14971 | RIBOSOMAL PROTEIN S9 |
| | NEGATIVE CONTROLS |

Oncogene and Tumor Suppressor Gene Array

In the oncogene and tumor suppressor gene array according to the subject invention, all of the unique polynucleotide probe compositions correspond to genes that are associated with cellular proliferative diseases, specifically neoplastic diseases. Genes of interest that
5 may be represented on the array include: oncogenes and tumor suppressor genes. In a specific oncogene and tumor suppressor gene array of interest, the spots are as provided in Table 6.

TABLE 6

| GenBank # | Gene Name |
|-------------------|--|
| V00568 | MYC PROTO-ONCOGENE PROTEIN |
| M29366 | HER3 (ERB-B3)[Epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)] |
| X04434 | INSULIN-LIKE GROWTH FACTOR I RECEPTOR |
| X03663 | MACROPHAGE COLONY STIMULATING FACTOR I RECEPTOR [c-fms proto-oncogene] |
| Z12020; [M92424] | MDM2 PROTEIN (P53-ASSOCIATED PROTEIN) + MDM2-A (GB: U33199) + MDM2-C (GB: U33201) |
| X02811; [X02744 ; | PLATELET-DERIVED GROWTH FACTOR, B CHAIN PRECURSOR (PDGF B-CHAIN) |
| M12783] | (PDGF-2) (BACAPLERMIN) (C-SIS) |
| X01394 | TUMOR NECROSIS FACTOR [TNFa] |
| K03222 | TRANSFORMING GROWTH FACTOR-ALPHA |
| X02812 | TRANSFORMING GROWTH FACTOR BETA [1] |
| M15024 | MYB PROTO-ONCOGENE PROTEIN |
| M14694 | CELLULAR TUMOR ANTIGEN P53 |
| M19154 | TRANSFORMING GROWTH FACTOR BETA [2] |
| X06182 | C-kit |
| L07594 | TGF-BETA RECEPTOR TYPE III |
| X07282 | RETINOIC ACID RECEPTOR BETA-2 |
| X13293 | MYB-RELATED PROTEIN B [B-myb] |
| M24898 | V-ERBA RELATED PROTEIN EAR-1 [Thyroid hormone triiodothyronine receptor c-erbA, ear-1] |
| K03193; [X00588; | EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112). (EGFR) |
| X00663; U48722] | (ERBB1) |
| X12794 | V-ERBA RELATED PROTEIN EAR-2 |
| X12795 | COUP TRANSCRIPTION FACTOR [V-erbA related ear-3 protein] |
| U11732 | ETS-RELATED PROTEIN TEL |
| U18422 | DP2 (Humdp2) , dimerization partner of E2F |
| L07868 | ERBB4 [EPIDERMAL GROWTH FACTOR RECEPTOR] |
| J04111 | TRANSCRIPTION FACTOR AP-1 [c-jun proto oncogene] |
| M33294 | TUMOR NECROSIS FACTOR RECEPTOR [Tumor necrosis factor receptor 1 (55kD)] |
| M11730 | ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE |

TABLE 6 (CONT)

| GenBank # | Gene Name |
|-----------------------------------|--|
| L12260 | HERGULIN ALPHA [Recombinant glial growth factor 2] |
| L12261 | HERGULIN ALPHA [Recombinant glial growth factor] |
| M27288 | ONCOSTATIN M |
| M59964 | STEM CELL FACTOR (C-KIT LIGAND) |
| M76125 | AXL (TYROSINE-PROTEIN KINASE RECEPTOR UFO) |
| X06182 | C-KIT PROTO-ONCOGENE [mas/stem cell growth factor receptor] |
| X06374 | PLATELET-DERIVED GROWTH FACTOR A CHAIN |
| D13866 | ALPHA-CATENIN |
| D17517 | SKY (DTK) (TYRO3) (RSE) |
| L11353; Z22664; X72657; L27133 | MERLIN (SCHWANNOMIN) (moesin-ezrin-radixin-like protein)(neurofibromatosis 2) |
| L13738 | TYROSINE-PROTEIN KINASE SYK [activated p21cdc42Hs kinase (ack)] |
| L14837 | TIGHT JUNCTION PROTEIN ZO-1 |
| L16785 | NUCLEOSIDE DIPHOSPHATE KINASE B [c-myc transcription factor (puf)] |
| L19067 | TRANSCRIPTION FACTOR P65 |
| L20422 | PROTEIN ETA [14-3-3 PROTEIN ETA] |
| L22075 | GUANINE NUCLEOTIDE REGULATORY PROTEIN (G13) |
| L25259 | T LYMPHOCYTE ACTIVATION ANTIGEN CD86 [CD28 antigen ligand 2, B7-2 antigen] |
| L33264 | CDC2-RELATED KINASE PISLRE |
| M13150 | MAS PROTO-ONCOGENE |
| M31213; [M57464] | PROTO-ONCOGENE TYROSINE-PROTEIN KINASE RECEPTOR RET PRECURSOR (EC 2.7.1.112) (C-RET).[Papillary thyroid carcinoma-encoded protein] |
| M31899 | DNA-REPAIR PROTEIN COMPLEMENTING XP-B CELLS [DNA repair helicase (ERCC3)] |
| M32865 | ATP-DEPENDENT DNA HELICASE II (70 KD SUBUNIT) [Thyroid autoantigen 70kD (Ku antigen)] |
| M34960 | TRANSCRIPTION FACTOR IID |
| M36089 | DNA-REPAIR PROTEIN XRCC1 |
| M54915 | PIM-1 PROTO-ONCOGENE (SERINE/THREONINE-PROTEIN KINASE) |
| M60915 | NEUROFIBROMIN [neurofibromatosis protein type I (NF1)] |
| M62397 | COLORECTAL MUTANT CANCER PROTEIN |

TABLE 6 (CONT)

| GenBank # | Gene Name |
|--------------------------|--|
| M62810 | MITF1 [TRANSCRIPTION FACTOR 1 MITOCHONDRIAL] |
| MB1750 | MYELOID CELL NUCLEAR DIFFERENTIATION ANTIGEN |
| MB1840 | TRANSFORMING PROTEIN MAF [NRL gene product] |
| MB3234 | Y BOX BINDING PROTEIN-1 [Nuclease-sensitive element DNA-binding protein] |
| U02082 | GUANINE NUCLEOTIDE REGULATORY PROTEIN TIM1 |
| U03056 | HYALURONIDASE [tumor suppressor (LUCA-1)] |
| U07236 | PROTO-ONCOGENE TYROSINE-PROTEIN KINASE LCK [Lymphocyte-specific protein tyrosine kinase] |
| U09579; [L25610] | CYCLIN-DEPENDENT KINASE INHIBITOR 1 (MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN 6) (MDA-6) (P21) (CDK-INTERACTING PROTEIN 1) (CIP1) (WAF1) (CDKN1A) (CDKN1) (SDI1) (PIC1) (CAP20) |
| X07024 | TRANSCRIPTION INITIATION FACTOR TFIIID (250 KD SUBUNIT) [CG1 protein inv. in cell proliferation] |
| X15218 | SKI ONCOGENE |
| X15219 | SKI-RELATED ONCOGENE SNON |
| X51630 | WILMS TUMOR PROTEIN |
| MB1933 | cdc25A; M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) |
| M92287 | CYCLIN D3 |
| S85655 | PROHIBITIN |
| X03484 | RAF PROTO-ONCOGENE (SERINE/THREONINE-PROTEIN KINASE) |
| X16416 | PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL |
| X59798; [M64349] | CYCLIN D1 (CYCLIN PRAD1) (BCL-1 ONCOGENE) |
| D13639 [M90813] | CYCLIN D2 |
| HT2291; [K03214; X03996] | PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC (EC 2.7.1.112) (P60-SRC) (C-SRC). |
| X75042 | C-REL PROTO-ONCOGENE PROTEIN |
| L25080 | TRANSFORMING PROTEIN RHOA [proto-oncogene rhoA, multidrug resistance protein] |
| X75342 | SHB ADAPTOR PROTEIN [A Src HOMOLOG 2 PROTEIN] |
| L26584 | CDC25 [GUANINE NUCLEOTIDE RELEASING PROTEIN] |
| X76132 | TUMOR SUPPRESSOR PROTEIN DCC |

TABLE 6 (CONT)

| GenBank # | Gene Name |
|------------------|---|
| L27211 | CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1) (CDKN2A) |
| M13228 | N-MYC PROTO-ONCOGENE PROTEIN |
| M15400 | RETINOBLASTOMA-ASSOCIATED PROTEIN [retinoblastoma susceptibility] |
| M15990 | PROTO-ONCOGENE TYROSINE-PROTEIN KINASE YES |
| M19720 | L-MYC-2 PROTEIN |
| M19722 | PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FGR (EC 2.7.1.112) (P55-FGR) (C-FGR) |
| M73812 | CYCLIN E (G1/S-SPECIFIC) |
| M74088 | ADENOMATOUS POLYPOSIS COLI PROTEIN |
| U25994 | TYROSINE-PROTEIN KINASE LYN [cell death protein RIP] |
| U40343; [U20498] | CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D) |
| U43746 | BREAST CANCER TYPE 2 SUSCEPTIBILITY PROTEIN |
| X02751 | TRANSFORMING PROTEIN P21 [N-ras] |
| X16706 | FRA-2 [fos-related antigen 2] |
| X16707 | FRA-1 [fos-related antigen 1] |
| X51521 | EZRIN [Villin 2] |
| X56681 | TRANSCRIPTION FACTOR JUN-D |
| X59932 | TYROSINE-PROTEIN KINASE CSK [C-SRC-kinase] |
| X86779 | FAST KINASE |
| X87838 | BETA-CATENIN |
| Z29090 | PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT ALPHA ISOFORM |
| M14745 | BCL2 |
| D38305 | TOB |
| L16464 | ETS-RELATED PROTEIN PE-1 [ETS oncogene (PEP1)] |
| L29216 | PROTEIN KINASE CLK (CLK2) |
| L29220 | PROTEIN KINASE CLK (CLK3) |
| L29222 | PROTEIN KINASE CLK (CLK1) |
| U10564 | CDK TYROSINE 15-KINASE WEE1Hu |

TABLE 6 (CONT)

| GenBank # | Gene Name |
|------------------|---|
| U22398 | CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITOR P57) (P57KIP2) |
| U24166 | EB1 |
| U26710 | PROTO-ONCOGENE C-CBL |
| U33841 | ATAXIA TELANGIECTASIA (ATM) |
| U35735 | RACH1 |
| U40282 | INTEGRIN-LINKED KINASE (ILK) [MIXED LINEAGE KINASE 2] |
| U41816 | C-1 |
| U43408 | FOCAL ADHESION KINASE [tyrosine kinase (Tnk1)] |
| U57456 | MOTHERS AGAINST DPP PROTEIN [chromosome 4 Mad homolog Smad1; transforming growth factor-beta signaling protein-1 (bsp-1)] |
| U60800 | semaphorin (CD100) |
| U61262 | TUMOR SUPPRESSOR PROTEIN DCC [neogenin] |
| U63139 | DNA REPAIR PROTEIN RAD50 |
| M81934; [S78187] | cdc25B; M-PHASE INDUCER PHOSPHATASE 2 (EC 3.1.3.48). (CDC25Hu2) |
| U17075; [L36844] | CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B) (MULTIPLE TUMOR SUPPRESSOR 2) (MTS2) (CDKN2B). |
| U84119 | LACTOFERRIN (DELTA) |
| X74262 | RBA/p48 |
| X85133 | RBQ1 retinoplastoma binding protein |
| Z29083 | ST4 ONCOFETAL ANTIGEN |
| L23959 | E2F-related transcription factor (DP-1) |
| L25676 | SERINE/THREONINE PROTEIN KINASE PITALRE |
| L26081 | semaphorin III |
| L37882 | frizzled |
| L20861 | Wnt-5a |
| M29039 | jun B TRANSACTIVATOR |
| M34065 | cdc25C; M-PHASE INDUCER PHOSPHATASE 3 (EC 3.1.3.48). |
| M73980 | Notch1 |
| M95712 | raf.b. |
| M99437 | notch group protein (N) |
| U15642 | E2F-5 |
| U33920 | semaphorin V |

TABLE 6 (CONT)

| GenBank # | Gene Name |
|------------------|--|
| U43318 | frizzled 5 |
| U46461 | dishevelled homolog (DVL) |
| U49262; [U75651] | dishevelled (DVL) + dishevelled 3 (DVL3) |
| L34075 | FKBP-RAPAMYSLIN ASSOCIATED PROTEIN (FRAP) |
| X07876 | WNT2 OR IRP |
| L40027 | glycogen synthase kinase 3 |
| X66360 | SERINE/THREONINE-PROTEIN KINASE PCTAIRE-2 |
| X66362 | SERINE/THREONINE-PROTEIN KINASE PCTAIRE-3 |
| X66363 | SERINE/THREONINE-PROTEIN KINASE PCTAIRE-1 |
| X74594 | RB2/p130 |
| X85134 | RBQ-3 |
| Z71621 | Wnt-13 |
| AB000220 | semaphorin E |
| AF001954 | growth inhibitor p33ING1 (ING1) |
| AF007111 | MDM2-like p53-binding protein (MDMX) |
| D89667 | C-myc binding protein |
| U29343 | HYALURONAN RECEPTOR (RHAMM) |
| U66469 | p53-dependent cell growth regulator CGR19 |
| U76638 | BRCA1-ASSOCIATED RING DOMAIN PROTEIN |
| U82169 | frizzled homolog (FZD3) |
| U84401 | smoothened |
| U90875 | cytotoxic ligand TRAIL- receptor |
| U95299 | Notch4 |
| Y11416 | p73, a monoallelically expressed p53-related protein |
| X91940 | WNT-8B |
| X97057 | WNT-10B |
| Y10479 | E2F-3 |
| Y11306 | beta catenin/TCF-4 |
| U38276 | SEMAPHORIN-1 |
| U77493 | Notch2 |
| K00650 | C-fos |
| X53795 | CD82 ANTIGEN (INDUCIBLE MEMBRANE PROTEIN R2) (C33 ANTIGEN) (IA4) (METASTASIS SUPPRESSOR KANGAI 1) (SUPPRESSOR OF TUMORIGENICITY-6). |
| L38518 | sonic hedgehog (Shh) |
| M54968 | K-RAS, ONCOGENE |

TABLE 6 (CONT)

| GenBank # | Gene Name |
|-----------------------------|---|
| M63167 | Akt1 (rac protein kinase alpha, protein kinase B, c-Akt) |
| S57153; S57160 | RBP1(RETINOBLASTOMA-BINDING PROTEIN) |
| U23435; U31089 | Abl interactor 2 (Abl-2) + Abl binding protein 3 (AblBP3) [ArgBP1B] |
| M96577 | E2F-1 pRB-binding protein |
| U24163; [U91903; U68057] | frizzled-related FrzB (Fritz) (frezzled (fre)) |
| L05148 | TYROSINE-PROTEIN KINASE ZAP-70 (EC 2.7.1.112) (70 KD ZETA-ASSOCIATED PROTEIN) (ZAP70) |
| M97935 | SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA (TRANSCRIPTION FACTOR ISGF-3 COMPONENTS P91/P84) (STAT1) |
| U10087 X58957 | TYROSINE-PROTEIN KINASE BTK (EC 2.7.1.112) (BRUTON'S TYROSINE KINASE)(AGAMMAGLOBULINAEMIA TYROSINE KINASE) (ATK) (B CELL PROGENITOR KINASE) (BPK) (BTK) (AGMX1) |
| AF016268 | death receptor 5 (DR5) |
| M35296 | TYROSINE-PROTEIN KINASE ABL2 (EC 2.7.1.112) (TYROSINE KINASE ARG) (ABL) |
| U18671 M97934 | SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 2 (P113) (STAT2) |
| U47686 | SIGNAL TRANSDUCER AND TRANSCRIPTION ACTIVATOR 5B (STAT5B) |
| M80629 | CDC2-RELATED PROTEIN KINASE CHED |
| S66431 | RBP2 retinoblastoma binding protein |
| U04045; [L47583] | DNA MISMATCH REPAIR PROTEIN MSH2 |
| U29656 | DR-NM23 |
| U43148 | patched homolog (PTC) |
| J02958 | MET |
| U49089 | neuroendocrine-dlg (NE-dlg) a novel human homolog of the Drosophila discs large (dlg) tumor suppressor protein interacting with the APC protein |
| U54777 | DNA MISMATCH REPAIR PROTEIN MSH6 (mutS - ALPHA 160 KD SUBUNIT) (G/T MISMATCH BINDING PROTEIN) (GTBP) (GTMBP) (P160) |
| X66358 | SERINE/THREONINE-PROTEIN KINASE KKIALRE |

Cell-Cell Interaction Array

In the cell-cell interaction array according to the subject invention, all of the unique polynucleotide probe compositions correspond to genes that are associated with cell-cell interaction, e.g. cell-cell signaling. In a specific cell-cell interaction array of interest, the

5 spots are as provided in Table 7.

TABLE 7

| GenBank # | CELL INTERACTION (Gene Names) |
|-----------------------------------|--|
| M32315 | TUMOR NECROSIS FACTOR RECEPTOR [Tumor necrosis factor receptor 2] |
| X01394 | TUMOR NECROSIS FACTOR [TNFa] |
| D12614 | LYMPHOTOXIN-ALPHA [formerly tumor necrosis factor beta [TNF-beta]] |
| M12807 | T-CELL SURFACE GLYCOPROTEIN CD4 |
| M14648 | VITRONECTIN RECEPTOR ALPHA [Integrin, alpha V; antigen CD51] |
| X75208 | TYROSINE-PROTEIN KINASE RECEPTOR EPH-3 |
| X74764 | TYROSINE-PROTEIN KINASE CAK [Tyrosine kinase, receptor TKT] |
| M18391 | TYROSINE-PROTEIN KINASE RECEPTOR EPH |
| U08839 [M83246; X51675] | UROKINASE PLASMINOGEN ACTIVATOR SURFACE RECEPTOR, GPI-ANCHORED FORM PRECURSOR (U-PAR) (MONOCYTE ACTIVATION ANTIGEN MO3) (CD87 ANTIGEN) |
| M33294 | TUMOR NECROSIS FACTOR RECEPTOR [Tumor necrosis factor receptor 1 (55kD)] |
| Y00285 | CATION-INDEPENDENT MANNANOSE-6-PHOSPHATE RECEPTOR [insuline-like growth factor receptor II, IGF-R-2] |
| L07414 | CD40 |
| L08096; | CD27 (CD70 ANTIGEN) |
| [S69339] | |
| L09753 | CD30 |
| M35410 | IGFBP-2 [INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2] |
| M63928 | CD27L RECEPTOR [T cell activation antigen (CD27)] |
| M67454 | FASL RECEPTOR [Fas antigen, APO-1 antigen] |
| M83554 | CD30L RECEPTOR [Lymphocyte activation antigen CD30; Ki-1 antigen] |
| X60592 | CD40L RECEPTOR [Cdw40 nerve growth factor receptor-related B-lymphocyte activation molecule] |
| D13866 [D14705 L23805; L22080] | ALPHA-CATENIN (CADHERIN-ASSOCIATED PROTEIN) (ALPHA E-CATENIN) |
| D25303; | integrin alpha9 |
| [L24158] | |
| J03132 | INTERCELLULAR ADHESION MOLECULE-1 |
| J04536 | LEUKOSIALIN [sialophorin (CD43)] |
| L11353; Z22664; | MERLIN (SCHWANNOMIN) (moesin-ezrin-radixin-like protein)(neurofibromatosis 2) |
| X72657; L27133 | |
| L13616 | Focal adhesion kinase |
| L14837 | TIGHT JUNCTION PROTEIN ZO-1 |
| L16785; | NUCLEOSIDE DIPHOSPHATE KINASE B (EC 2.7.4.6) (NDK B) (NDP KINASE B) (NM23-H2) |
| [M36981] | (C-MYC PURINE-BINDING TRANSCRIPTION FACTOR PUF). |

TABLE 7 (CONT)

| GenBank # | CELL INTERACTION (Gene Names) |
|---------------------------------|---|
| L20815 | S PROTEIN |
| L25259 | T LYMPHOCYTE ACTIVATION ANTIGEN CD86 [CD28 antigen ligand 2, B7-2 antigen] |
| L34774 | opioid binding cell adhesion molecule |
| M15476 | UROKINASE-TYPE PLASMINOGEN ACTIVATOR PRECURSOR (EC 3.4.21.73) (UPA) (U-PLASMINOGEN ACTIVATOR) |
| M15518; [X07393; M18182] | TISSUE-TYPE PLASMINOGEN ACTIVATOR PRECURSOR (EC 3.4.21.68) (T-PA) (T-PLASMINOGEN ACTIVATOR). |
| M18082; [J02685] | PLASMINOGEN ACTIVATOR INHIBITOR-2, PLACENTAL (PAI-2) (MONOCYTE ARG-SERPIN) (UROKINASE INHIBITOR). |
| M21097 | CD19 B-LYMPHOCYTE ANTIGEN [Differentiation antigen (CD19)] |
| M23197 | CD33 MYELOID CELL SURFACE ANTIGEN [Differentiation antigen (CD33)] |
| M28882 | CELL SURFACE GLYCOPROTEIN MUC18 |
| M30257 | VASCULAR CELL ADHESION PROTEIN [vascular cell adhesion molecule 1] |
| M30640 | E-SELECTIN [Endothelial leucocyte adhesion molecule 1 (ELAM1)] |
| M34064 [X57548; X54315; S42303] | CADHERIN-2 (N-CADHERIN) |
| M54992 | CD72 B-CELL DIFFERENTIATION ANTIGEN |
| M59040 | CD44 ANTIGEN HEMATOPOIETIC FORM [Cell adhesion molecule (CD44)] |
| M63618 | bullous pemphigoid antigen |
| M74387 | L1CAM |
| M74777 | CD26 [DIPEPTIDYL PEPTIDASE IV; adenosine deaminase complexing protein 2] |
| U01160 | SAS (TRANSMEMBRANE 4 SUPERFAMILY PROTEIN) |
| U03056 | HYALURONIDASE [tumor suppressor (LUCA-1)] |
| U07819 | CONTACTIN [Contactin 1 (CNTN1)] |
| U15979 | DELTA-LIKE PROTEIN [dlk] |
| X16841 | N-CAM [NEURAL CELL ADHESION MOLECULE, PHOSPHATIDYLINOSITOL-LINKED ISOFORM; CD56] |
| X70326 | MacMarcks |
| X74979 | TYROSINE-PROTEIN KINASE CAK [EDDR1; TRK E] |
| Z26317 [S64273] | desmoglein 2 |
| L25080 | TRANSFORMING PROTEIN RHOA [proto-oncogene rhoA, multidrug resistance protein] |
| X76132 | DCC |
| J02703 | PLATELET MEMBRANE GLYCOPROTEIN IIIA |

TABLE 7 (CONT)

| GenBank # | CELL INTERACTION (Gene Names) |
|-----------|--|
| J04145 | INTEGRIN ALPHA M [Neutrophil adherence receptor alpha-M subunit; Complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide] |
| J05633 | integrin beta5 |
| L12002; | integrin alpha4 |
| [X16983] | |
| L25851 | integrin alphaE |
| L3531 | integrin alpha8 |
| M15395 | LEUKOCYTE ADHESION PROTEIN [CELL SURFACE ADHESION GLYCOPROTEINS LFA-1, CR3 AND P150,95, BETA-SUBUNIT] |
| M28249; | integrin alpha2 [very late antigen-2 (Vla-2)/collagen receptor alpha-2 subunit] |
| [X17033] | |
| M34480 | INTEGRIN ALPHA 2B [PLATELET MEMBRANE GLYCOPROTEIN IIB (GPIIb); antigen CD41B] |
| M35198 | integrin beta6 |
| M59911 | integrin alpha3 |
| M62880 | integrin beta7 |
| M73780 | integrin beta8 |
| M81695 | INTEGRIN ALPHA X [LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN; antigen CD11C (p150)] |
| X06256 | integrin alpha5 [fibrinectin receptor alpha subunit] |
| X07979 | FIBRONECTIN RECEPTOR (BETA SUBUNIT) [INTEGRIN BETA 1] |
| X53586; | integrin alpha6 |
| [X59512] | |
| X53587; | integrin beta4 |
| [X52186] | |
| X68742 | integrin alpha |
| X74295 | integrin alpha7B |
| Y00796 | INTEGRIN ALPHA L [LEUKOCYTE ADHESION GLYCOPROTEIN LFA-1 ALPHA CHAIN; antigen CD11A (p180)] |
| D38122 | FAS ANTIGEN LIGAND |
| M74088; | APC (DP2.5) |
| [M73548] | |
| U43522; | Protein tyrosine kinase Pyk2 (Cell adhesion kinase-beta, CAK-beta) (FAK2) |
| [L49207] | |
| X51521 | Ezrin (cytovillin 2) |

TABLE 7 (CONT)

| GenBank # | CELL INTERACTION (Gene Names) |
|------------------|--|
| X87838 [Z19054] | BETA-CATENIN |
| L11015 | LYMPHOTOXIN-BETA |
| U57059 | FAS ANTIGEN LIGAND [TNF-related apoptosis inducing ligand TRAIL; Apo-2 ligand] |
| D45132 | ANNEXIN 1 [zinc finger protein RIZ] |
| M68516; | PLASMA SERINE PROTEASE INHIBITOR PRECURSOR (PCI) (PROTEIN C INHIBITOR) |
| [J02639] | (PLASMINOGEN ACTIVATOR INHIBITOR-3) (PAI3). |
| U40282 | Integrin-linked kinase (ILK) |
| U43408 | FOCAL ADHESION KINASE [tyrosine kinase (Tnk1)] |
| U60800 | semaphorin (CD100) |
| U61262 | TUMOR SUPPRESSOR PROTEIN DCC [neogenin] |
| L11370 | protocadherin 42 |
| X78817 | RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131). |
| X85978 | TAX1, AXONIN-1/TAQ1 |
| L11373 | protocadherin 43 |
| X89576 | MMP-17 (MT4-MMP) |
| Y00815 | LAR |
| Z30183 | TIMP-3 [mitogen-inducible gene 5, mig-5] |
| Z35227 | ras-like small GTPase TTF |
| D26512, | MMP-14 (MT1-MMP) |
| [X83535] | |
| D31784 | CADHERIN-6 |
| D50477 | MMP-16 (MT3-MMP) |
| D83542 | CADHERIN-14 MUSCLE-CADHERIN PRECURSOR (M-CADHERIN) (CADHERIN-14) (CADHERIN-15) |
| J03210, [J05471] | MMP-2 (gelatinase A) |
| J05070, [D10051] | MMP-9 (gelatinase B) |
| J05556 | MMP-8 (collagenase-2) |
| L20688 | rho GDP-dissociation inhibitor protein 2 (Ly-GDI) |
| L26081 | semaphorin III |
| L34056 | CADHERIN-11 (OSTEOBLAST-CADHERIN) (OB-CADHERIN) |
| L34057; [L33477] | CADHERIN-12 (BR-CADHERIN) (N-CADHERIN 2) (CADHERIN, NEURAL TYPE, 2) |

TABLE 7 (CONT)

| GenBank # | CELL INTERACTION (Gene Names) |
|-----------|---|
| L34058; | CADHERIN-13 T-CADHERIN PRECURSOR (TRUNCATED-CADHERIN) (H-CADHERIN) |
| [U59288; | (HEART-CADHERIN) |
| U59288] | |
| L34059 | CADHERIN-4 RETINAL-CADHERIN PRECURSOR (R-CADHERIN) (R-CAD) |
| L34060 | CADHERIN-8 |
| M23410 | PLAKOGLOBIN (DESMOPLAKIN III) |
| M94151 | ALPHA-CATENIN RELATED PROTEIN (CATENIN ALPHA-2) |
| U24152 | SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA (EC 2.7.1.1) (P65-PAK) (P21- ACTIVATED KINASE) (ALPHA-PAK) |
| U24153 | p21-activated protein kinase (Pak2) |
| U33920 | semaphorin V |
| U43318 | frizzled 5 |
| X04429 | PLASMINOGEN ACTIVATOR INHIBITOR-1 PRECURSOR, ENDOTHELIAL (PAI-1) |
| X13916 | LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MACROGLOBULIN RECEPTOR) (A2MR) |
| X14787 | THROMBOSPONDIN 1 PRECURSOR |
| L40027 | glycogen synthase kinase 3 |
| X54412 | collagen type IX alpha-1 |
| X56654 | desmoglein type 1 |
| X56807 | DSC2 mRNA for desmocollins type 2a and 2b |
| X61587 | rhoG |
| X63629 | CADHERIN-3 PLACENTAL-CADHERIN PRECURSOR (P-CADHERIN) |
| X69550 | rho GDP-dissociation inhibitor 1 |
| X75308 | MMP-13 (collagenase-3) |
| X78565 | TENASCIN-C |
| X79981; | CADHERIN-5 VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (7B4 |
| [X59796] | ANTIGEN) (CD144 ANTIGEN). |
| M11313 | ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M) |
| X95282 | Rho8 protein |
| X95456 | Rho7 protein |
| Y07923 | Rho6 protein |
| Z13009 | CADHERIN-1(E-CADHERIN) (UVOMORULIN) (CAM 120/80) |
| Z15009 | laminin |
| Z48482 | MMP-15 (MT2-MMP) |
| AB000220 | semaphorin E |
| AF003522 | Delta |

TABLE 7 (CONT)

| GenBank # | CELL INTERACTION (Gene Names) |
|-----------|---|
| D85815 | rho-HP1 |
| AF000974 | Zyxin related protein ZRP-1 |
| U29343 | HYALURONAN RECEPTOR (RHAMM) |
| M24795 | PLATELET GLYCOPROTEIN IV (GPV) (GPIIB) (CD36 ANTIGEN) (PAS IV) (PAS-4 PROTEIN) |
| U72661 | NINJURIN-1 |
| U76456 | TIMP-4 |
| U82532 | GDI-dissociation inhibitor RhoGDIgamma |
| X92521 | MMP-19 |
| Y07604 | nm23-H4; NUCLEOSIDE-DIPHOSPHATE KINASE (EC 2.7.4.6) (NUCLEOSIDE 5'-DIPHOSPHATE PHOSPHOTRANSFERASE) (NDK). |
| Y11306 | beta catenin/TCF-4 |
| U38276 | SEMAPHORIN-1 |
| U94354 | lunatic fringe |
| U02570 | CDC42 GTPase-activating protein |
| X05199 | PLASMINOGEN PRECURSOR (EC 3.4.21.7) |
| X05231 | MMP-1 (collagenase-1) |
| X53795 | CD82 ANTIGEN (INDUCIBLE MEMBRANE PROTEIN R2) (C33 ANTIGEN) (IA4) (METASTASIS SUPPRESSOR KANGAI 1) (SUPPRESSOR OF TUMORIGENICITY-6). |
| L38517 | indian hedgehog protein (IHH) |
| M31470 | ras-like protein TC10 |
| M34189 | integrin beta1 |
| X83929; | desmocollin type 3 + desmocollin type 4 |
| D174271 | |
| L23808 | MMP-12 (matrilysinase) |
| L25081 | rhoC (H9); SMALL GTPase (rhoC) |
| M29870; | RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 (P21-RAC1) (RAS-LIKE PROTEIN TC25) |
| M64595; | RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 (P21-RAC2) |
| [M29871] | |
| X05232 | MMP-3 (stromelysin-1) |
| X06820 | rhoB |
| X07820; | MMP-10 (stromelysin-2) |
| [M30461] | |
| X72925 | desmocollin type 1 |

TABLE 7 (CONT)

| GenBank # | CELL INTERACTION (Gene Names) |
|----------------|---|
| X94991; | Zyxin + Zyxin-2 |
| [X95735] | |
| U52111 | PLEXIN |
| M38690 | CD9 |
| M54995; M38441 | PLATELET BASIC PROTEIN PRECURSOR (PBP) (CONTAINS: CONNECTIVE-TISSUE ACTIVATING PEPTIDE III (CTAP-III), LOW-AFFINITY PLATELET FACTOR IV (LA-PF4), BETA-THROMBOGLOBULIN (BETA-TG), NEUTROPHIL-ACTIVATING PEPTIDE 2 (NAP-2)) |
| L20471 | extracellular matrix metalloproteinase inducer EMMPRIN |
| M57730 M37476 | EPHRIN-A1 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 1) (LERK-1) (IMMEDIATE EARLY RESPONSE PROTEIN B61) (TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 4). |
| U07695 | EPHRIN TYPE-B RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR HTK). |
| U09304 | EPHRIN-B1 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 2) (LERK-2) (ELK LIGAND PRECURSOR) (ELK-L). |
| U41766 | metalloproteinase/disintegrin/cysteine-rich protein precursor (MDC9) |
| U26403 | EPHRIN-A5 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 7) (LERK-7) (AL-1). |
| AF035752 | caveolin-2 |
| U32114 | |
| U66406 | EPHRIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 8) (LERK-8) (EPH-RELATED RECEPTOR TRANSMEMBRANE LIGAND ELK-L3). |
| X95425 | EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-1) (EPH HOMOLOGY KINASE-1) (RECEPTOR PROTEIN-TYROSINE KINASE HEK7). |
| Z18951 S49856 | caveolin-1 |
| L38734 | EPHRIN-B2 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 5) (LERK-5) (HTK LIGAND) (HTK-L). |
| L40636 | EPHRIN TYPE-B RECEPTOR 1 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EPH-2) (NET). |
| L41939 | EPHRIN TYPE-B RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN EPH-3) (ORT) |
| M16591 | TYROSINE-PROTEIN KINASE HCK (EC 2.7.1.112) (P59-HCK AND P60-HCK) (HEMOPOIETIC CELL KINASE). |

TABLE 7 (CONT)

| GenBank # | CELL INTERACTION (Gene Names) |
|---------------|--|
| M59371 M36395 | EPHRIIN TYPE-A RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ECK) (EPITHELIAL CELL KINASE). |
| M63959 | ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN PRECURSOR (ALPHA-2-MRAP) (LOW DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN- ASSOCIATED PROTEIN 1) (RAP) |
| M77830 | desmoplakin 1 |
| M86826 | IGF BINDING PROTEIN ACID-LABILE SUBUNIT |
| M99487 | PROSTATE-SPECIFIC MEMBRANE ANTIGEN (PSM) |
| U04441 | LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2 (MEGALIN) (GLYCOPROTEIN 330) (FRAGMENT) |
| U11690 | PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR(RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN) |
| U14588 | Paxillin |
| U16296 | T-lymphoma invasion and metastasis inducing TIAM1 |
| U29656 | DR-NM23 |
| U32907 | P37NB |
| U35113 | METASTASIS-ASSOCIATED MTA1 |
| U37139 | beta 3-endonexin |
| U43195 | Rho-associated, coiled-coil containing protein kinase p160ROCK |
| U43527 | malignant melanoma metastasis-suppressor (KiSS-1) gene |
| U49089 | neuroendocrine-dlg (NE-dlg) a novel human homolog of the Drosophila discs large (dlg) tumor suppressor protein interacting with the APC protein |
| U53786 | envoplakin (EVPL) |
| U59752 | cytohesin-1; Sec7p-like protein |
| X03124 | TIMP-1 (erythroid potentiating activity, EPA) |
| X07819 | MMP-7 (matrilysin) |
| X17620 | NUCLEOSIDE DIPHOSPHATE KINASE A (EC 2.7.4.6) (NDK A) (NDP KINASE A) (TUMOR METASTATIC PROCESS-ASSOCIATED PROTEIN) (METASTASIS INHIBITION FACTOR NM23) (NM23-H1). |
| J05593 | TIMP-2 (M1) |
| X57766 | MMP-11 (stromelysin-3) |

Cytokine and Cytokine Receptor Array

In the cytokine and cytokine receptor array according to the subject invention, all of the unique polynucleotide probe compositions correspond to genes that express cytokines or cytokine receptors. In a specific cytokine and cytokine receptor array of interest, the spots

5 are as provided in Table 8.

TABLE 8

| GenBank # | Gene Name |
|-----------|---|
| M29696 | INTERLEUKIN-7 RECEPTOR ALPHA CHAIN |
| X01992 | INTERFERON GAMMA |
| J04156 | INTERLEUKIN-7 |
| X01057 | INTERLEUKIN-2 RECEPTOR ALPHA CHAIN |
| A14844 | INTERLEUKIN-2 |
| M29366 | PROTEIN-TYROSINE KINASE RECEPTOR ERBB-3 (Epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)) |
| X04434 | INSULIN-LIKE GROWTH FACTOR I RECEPTOR |
| M29645 | INSULIN-LIKE GROWTH FACTOR II [Somatomedin A] |
| X03663 | MACROPHAGE COLONY STIMULATING FACTOR I RECEPTOR [c-fms proto-oncogene] |
| M32315; | TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR |
| [M55994] | BINDING PROTEIN 2) (TBPI) (P80) (TNF-R2) (P75) (CD120B) (TNFR2) (TNFR) |
| X02811; | PLATELET-DERIVED GROWTH FACTOR, B CHAIN PRECURSOR (PDGF B-CHAIN) |
| [X02744; | (PDGF-2) (BACAPLERMIN) (C-SIS) |
| M12783] | |
| X02851 | INTERLEUKIN-1 ALPHA |
| K02770 | INTERLEUKIN IL-1BETA |
| M14743; | INTERLEUKIN-3 PRECURSOR (IL-3) (MULTIPOTENTIAL COLONY-STIMULATING |
| [M17115] | FACTOR) (HEMATOPOIETIC GROWTH FACTOR) (P-CELL STIMULATING FACTOR) |
| | (MAST-CELL GROWTH FACTOR) (MCGF) (IL3). |
| M13982 | INTERLEUKIN-4 |
| X04602; | INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) |
| [M14584] | (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR). |
| X01394 | TUMOR NECROSIS FACTOR [TNF α] |
| D12614 | LYMPHOTOXIN-ALPHA [formerly tumor necrosis factor beta (TNF-beta)] |
| M20566 | INTERLEUKIN-6 RECEPTOR ALPHA CHAIN |
| X04686; | INTERLEUKIN IL-5 (B CELL DIFFERENTIATION FACTOR 1) (T-CELL REPLACING |
| [J03478] | FACTOR) (EOSINOPHIL DIFFERENTIATION FACTOR) |
| M28622 | INTERFERON BETA |
| M11220 | GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR [GM-CSF] |
| K03222 | TRANSFORMING GROWTH FACTOR-ALPHA |
| J00209; | LEUKOCYTE INTERFERON ALPHA |
| [J00207] | |
| X02812 | TRANSFORMING GROWTH FACTOR BETA [1] |
| X03438 | GRANULOCYTE COLONY-STIMULATING FACTOR [G-CSF] |
| M19154 | TRANSFORMING GROWTH FACTOR BETA [2] |
| X04571 | EPIDERMAL GROWTH FACTOR KIDNEY [EGF] |
| J03171 | HUIEN-ALPHA-REC [INTERFERON ALPHA-BETA RECEPTOR ALPHA CHAIN] |
| M57627 | INTERLEUKIN-10 |
| M26062 | INTERLEUKIN-2 RECEPTOR BETA CHAIN |

TABLE 8 (CONT)

| GenBank # | Gene Name |
|-----------|--|
| M74782 | INTERLEUKIN-3 RECEPTOR ALPHA CHAIN |
| X52425 | INTERLEUKIN-4 RECEPTOR ALPHA CHAIN |
| M75914 | INTERLEUKIN-5 RECEPTOR ALPHA CHAIN |
| X77722 | INTERFERON ALPHA-BETA RECEPTOR BETA CHAIN |
| X72755 | GAMMA INTERFERON INDUCED MONOKINE [Humig] |
| D11086 | CYTOKINE RECEPTOR COMMON GAMMA CHAIN [Interleukin 2 receptor gamma chain] |
| M20132 | ANDROGEN RECEPTOR |
| M73238 | CILIARY NEUROTROPHIC FACTOR RECEPTOR ALPHA |
| J03143 | INTERFERON-GAMMA RECEPTOR ALPHA CHAIN |
| M60459 | ERYTHROPROTEIN RECEPTOR |
| L00587 | CALCITONIN RECEPTOR |
| M62424 | THROMBIN RECEPTOR [Coagulation factor II (thrombin) receptor] |
| L07594 | TRANSFORMING GROWTH FACTOR-BETA TYPE III RECEPTOR |
| M84747 | INTERLEUKIN-9 RECEPTOR |
| U00672 | INTERLEUKIN-10 RECEPTOR |
| M14764 | LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR |
| X60957 | TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR (EC 2.7.1.112). |
| [S89716] | VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (VEGFR-3) (TYROSINE-PROTEIN KINASE RECEPTOR FLT4, CLASS III). |
| X68203; | |
| [X69878; | |
| U43143] | |
| M16552 | THROMBOMODULIN |
| M87290 | ANGIOTENSIN II RECEPTOR TYPE-1A |
| M83941 | TYROSINE-PROTEIN KINASE RECEPTOR ETK1 |
| M76673 | FMLP-RELATED RECEPTOR 1 |
| M97675 | TRANSMEMBRANE RECEPTOR ROR1 |
| L04947; | VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (VEGFR-2) (KDR) (KINASE INSERT DOMAIN RECEPTOR) (FRAGMENT) |
| [X61656] | INTERFERON CONSENSUS SEQUENCE BINDING PROTEIN [DNA-binding protein] |
| M91196 | TYROSINE-PROTEIN KINASE RECEPTOR EPH-3 |
| X75208 | Irk-C |
| U05012 | TYROSINE-PROTEIN KINASE CAK [Tyrosine kinase, receptor TKI] |
| X74764 | EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112). (EGFR) |
| K03193; | (ERBB1) |
| [X00588; | |
| X00663; | |
| U48722] | PLATELET ACTIVATING FACTOR RECEPTOR |
| D10202 | TYROSINE-PROTEIN KINASE RECEPTOR EPH |
| M18391 | INTERFERON-GAMMA RECEPTOR |
| A09781 | TYROSINE KINASE RECEPTOR TRK-B |
| U12140 | |

TABLE 8 (CONT)

| GenBank # | Gene Name |
|-----------|--|
| M86492 | GLIA MATURATION FACTOR BETA |
| L07868 | ERBB4 [EPIDERMAL GROWTH FACTOR RECEPTOR] |
| M27492 | INTERLEUKIN-1 RECEPTOR TYPE I |
| M33294 | TUMOR NECROSIS FACTOR RECEPTOR 1 |
| M37435 | MACROPHAGE COLONY STIMULATING FACTOR-1 [M-CSF] |
| M11730 | ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE |
| D10923 | HM74 [PROBABLE G PROTEIN-COUPLED RECEPTOR HM74] |
| D10924 | HM89 [PROBABLE G PROTEIN-COUPLED RECEPTOR LCRT HOMOLOG] |
| D10925 | HM145 [C-C CHEMOKINE RECEPTOR TYPE 1] |
| D14012 | HEPATOCYTE GROWTH FACTOR ACTIVATOR |
| D16431 | HEPTOMA-DERIVED GROWTH FACTOR |
| D30751; | BONE MORPHOGENETIC PROTEIN 4 (BMP-2B) |
| [M22490] | |
| J03358 | PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FER |
| J04130 | MACROPHAGE INFLAMMATORY PROTEIN 1-BETA [Activation (Act-2)] |
| J05081 | ENDOTHELIN-3 |
| L06139 | TYROSINE-PROTEIN KINASE RECEPTOR TIE-2 PRECURSOR (EC 2.7.1.112) (TYROSINE PROTEIN KINASE RECEPTOR TEK) (P140 TEK) (TUNICA INTERNA ENDOTHELIAL CELL KINASE) |
| L06622 | ENDOTHELIN-1 RECEPTOR [EDNRA] |
| L06623 | ENDOTHELIN B RECEPTOR [EDNRB] |
| L06801 | INTERLEUKIN-13 |
| L07414 | CD40 LIGAND |
| L08096 | CD27 LIGAND [CD70 antigen] |
| L08187 | CILIARY NEUROTROPHIC FACTOR RECEPTOR ALPHA [cytokine receptor EB13] |
| L09753 | CD30 |
| L12260; | RECOMBINANT GLIAL GROWTH FACTOR + NEU DIFFERENTIATION FACTOR + |
| U02326; | HEREGULIN |
| M94165 | |
| L12261 | HEREGULIN ALPHA [Recombinant glial growth factor] |
| L15344 | INTERLEUKIN IL-14 |
| L36052; | THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING |
| [L36051; | FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT |
| U11025] | FACTOR) (MGDF) (THPO) |
| M10051 | INSULIN RECEPTOR |
| M21121 | RANTES PROTEIN T-CELL SPECIFIC |
| M21574 | PLATELET-DERIVED GROWTH FACTOR RECEPTOR ALPHA |
| M21616 | PLATELET-DERIVED GROWTH FACTOR RECEPTOR BETA |
| M22488; | BONE MORPHOGENETIC PROTEIN 1 (procollagen C-proteinase) (pCP-2) |
| [U50330] | |
| M22489 | BONE MORPHOGENETIC PROTEIN 2A |

TABLE 8 (CONT)

| GenBank # | Gene Name |
|--------------|---|
| M22491 | BONE MORPHOGENETIC PROTEIN 3 |
| M23452 | MACROPHAGE INFLAMMATORY PROTEIN 1-ALPHA [GOS19-1] |
| M24545 | MONOCYTE CHEMOTACTIC PROTEIN 1 |
| M25667 | NEUROMODULIN [Neuronal growth protein 43 (GAP-43)] |
| M27288 | ONCOSTATIN M |
| M30704 | AMPHIREGULIN [schwannoma-derived growth factor] |
| M31145 | INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 |
| M31165 | TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 |
| M32977; | VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR |
| [M27281] | PERMEABILITY FACTOR) (VPF). |
| M35410 | IGFBP-2 [INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 |
| M36717 | PLACENTAL RIBONUCLEASE INHIBITOR [Ribonuclease/angiogenin inhibitor RA] |
| M37722; | BASIC FIBROBLAST GROWTH FACTOR RECEPTOR 1 PRECURSOR (BFGF-R) (EC |
| [X66945; | 2.7.1.12) (FMS-LIKE TYROSINE KINASE-2) (C-FGR) (FGFR1) (FLG) (FGFR) (FLT2). |
| M63887; | (HBGF-R-ALPHA-A1) (HBGF-R-ALPHA-A2) (HBGF-R-ALPHA-A3) + FGFR SECRETED |
| M63888; | FORM (M34188) |
| M63889;M3418 | |
| 6; M34641] | |
| M57230 | INTERLEUKIN-6 RECEPTOR BETA CHAIN [membrane glycoprotein gp130] |
| M57399; | PLEIOTROPHIN PRECURSOR (PTN) (HEPARIN-BINDING GROWTH-ASSOCIATED |
| [X52946; | MOLECULE) (HB-GAM) (HEPARIN-BINDING GROWTH FACTOR 8) (HBGF-8) |
| D90226] | (OSTEOBLAST SPECIFIC FACTOR 1) (OSF-1) (HEPARIN-BINDING NEURITE |
| | OUTGROWTH PROMOTING FACTOR 1) (HBNF-1). |
| M57502 | T LYMPHOCYTE-SECRETED PROTEIN 1-309 |
| M57765 | INTERLEUKIN-11 [adipogenesis inhibitory factor] |
| M59818 | GRANULOCYTE COLONY STIMULATING FACTOR RECEPTOR |
| M59964 | STEM CELL FACTOR (C-KIT LIGAND) |
| M60278 | HEPARIN-BINDING EGF-LIKE GROWTH FACTOR [DIPHThERIA TOXIN RECEPTOR] |
| M60718 | HEPATOCYTE GROWTH FACTOR PRECURSOR (SCATTER FACTOR) (SF) |
| | (HEPATOPOEITIN A). |
| M60828 | FGF-7; KERATINOCYTE GROWTH FACTOR PRECURSOR (KGF) (FIBROBLAST |
| | GROWTH FACTOR-7) (HBGF-7). |
| M61176 | BRAIN-DERIVED NEUROTROPHIC FACTOR |
| M62302 | GDF-1 [GROWTH/DIFFERENTIATION FACTOR 1] |
| M62505 | CSA ANAPHYLATOXIN CHEMOTACTIC RECEPTOR |
| M65199 | ENDOTHELIN-2 |
| M65290 | INTERLEUKIN-12 BETA CHAIN [Natural killer cell stimulatory factor, p40] |
| M65291 | INTERLEUKIN-12 ALPHA CHAIN [Natural killer cell stimulatory factor, p35] |
| M67454 | FASL RECEPTOR [Fas antigen, APO-1 antigen] |
| M68932 | INTERLEUKIN-8 RECEPTOR [ALFA, HIGH AFFINITY] |
| M73482 | NEUROMEDIN-B RECEPTOR |

TABLE 8 (CONT)

| GenBank # | Gene Name |
|-----------|--|
| M74178 | HEPATOCYTE GROWTH FACTOR-LIKE (macrophage-stimulating protein (MST1)) |
| M76125 | AXL (TYROSINE-PROTEIN KINASE RECEPTOR UFO) |
| M92381 | THYMOSIN BETA-10 |
| M92934 | CONNECTIVE TISSUE GROWTH FACTOR |
| M96956; | TDGF1 (TERATOCARCINOMA-DERIVED GROWTH FACTOR 1) (EPIDERMAL GROWTH |
| [M96955] | FACTOR-LIKE CRIPTO PROTEIN CR1) (CRIPTO-1 GROWTH FACTOR) (CRGF) + |
| | TDGF2 (TERATOCARCINOMA-DERIVED GROWTH FACTOR 2) (EPIDERMAL GROWTH |
| | FACTOR-LIKE CRIPTO PROTEIN CR3) (CRIPTO-3 GROWTH |
| S59184 | TYROSINE-PROTEIN KINASE RYK [RYK receptor-like tyrosine kinase] |
| U01134; | VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 PRECURSOR (EC |
| [X51602] | 2.7.1.112) (VEGFR-1) (TYROSINE-PROTEIN KINASE RECEPTOR FLT) (FLT-1) (SFLT) |
| U02687 | FL CYTOKINE RECEPTOR PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE |
| | RECEPTOR FLT3) (STEM CELL TYROSINE KINASE 1) (STK-1) (CD135 ANTIGEN). |
| U03187 | INTERLEUKIN-12 RECEPTOR |
| U03882 | C-C CHEMOKINE RECEPTOR [Monocyte chemoattractant protein 1 receptor (MCP-1RA) |
| | alternatively spliced] |
| U03905 | C-C CHEMOKINE RECEPTOR [Monocyte chemoattractant protein 1 receptor (MCP-1RB) |
| | alternatively spliced] |
| U04806; | SL CYTOKINE PRECURSOR (FLT3/FLK2 LIGAND). |
| [U03858] | |
| U10117 | ENDOTHELIAL-MONOCYTE ACTIVATING POLYPEPTIDE II |
| U11814; | FIBROBLAST GROWTH FACTOR RECEPTOR 2 PRECURSOR (FGFR-2) (EC 2.7.1.112) |
| [M80634; | (KERATINOCYTE GROWTH FACTOR RECEPTOR) (FGFR2) (BEK) (BFR-1) (KSAM-1) + K- |
| X52832; | SAM; K-SAM-III; K-SAM-IV |
| M35718; | |
| M87771; | |
| [M87772] | |
| U14407 | INTERLEUKIN-15 |
| U14722 | ACTIVIN TYPE I RECEPTOR |
| U43142 | VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C) (VASCULAR |
| | ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRP) (FLT4 LIGAND). |
| X06182 | C-KIT PROTO-ONCOGENE [mas/stem cell growth factor receptor] |
| X06233 | CALGRANULIN (B) [MRP-14 (calcium binding protein in macrophages, MIF-related)] |
| X06234 | CALGRANULIN (A) [MRP-8 (calcium binding protein in macrophages, MIF-related)] |
| X06374 | PLATELET-DERIVED GROWTH FACTOR (A CHAIN) [PDGF-A] |
| X13967 | LEUKAEMIA INHIBITORY FACTOR [cholinergic differentiation factor] |
| X17543 | INTERLEUKIN-9 |
| X17648 | GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR RECEPTOR ALPHA |
| | CHAIN [hGM-CSF-R] |

TABLE 8 (CONT)

| GenBank # | Gene Name |
|-----------|---|
| X51943; | HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA-ENDOTHELIAL CELL GROWTH FACTOR) (ECGF-BETA). |
| [M13361]; | |
| X65778] | |
| X53655; | NT-3 (NEUROTROPHIN-3 PRECURSOR) (NEUROTROPHIC FACTOR) (HDNF) (NERVE GROWTH FACTOR 2) (NGF-2). |
| [M37763] | |
| X53799 | MACROPHAGE INFLAMMATORY PROTEIN-2-ALPHA [MIP2alpha] |
| X54936 | PLACENTA GROWTH FACTORS 1 AND 2 PRECURSOR (PLGF-1 / PLGF-2). |
| X59770 | INTERLEUKIN-1 RECEPTOR TYPE II |
| X60592 | CDW40; NERVE GROWTH FACTOR RECEPTOR-RELATED B-LYMPHOCYTE ACTIVATION MOLECULE |
| X72304 | CORTICOTROPIN RELEASING FACTOR RECEPTOR |
| X78686 | NEUTROPHIL ACTIVATING PROTEIN ENA-78 |
| X79929 | OX40 LIGAND [gp34] |
| Y00787 | INTERLEUKIN-8 [monocyte-derived neutrophil chemotactic factor MDNCF] |
| Z70519 | FAS/APO 1 |
| D17517 | TYROSINE-PROTEIN KINASE RECEPTOR UFO [sky] |
| J03241 | TRANSFORMING GROWTH FACTOR (BETA 3) |
| J03634 | INHIBIN BETA (A CHAIN) [activin A, activin AB alpha polypeptide; erythroid differentiation protein mRNA (EDF)] |
| L32976 | PROTEIN KINASE MLK-3 [MIXED LINEAGE KINASE 1] |
| L35233 | AUTOCRINE MOTILITY FACTOR RECEPTOR [AMFR] |
| M31213; | PROTO-ONCOGENE TYROSINE-PROTEIN KINASE RECEPTOR RET PRECURSOR (EC 2.7.1.112) (C-RET) [Papillary thyroid carcinoma-encoded protein] |
| [M57464] | |
| M95489 | FOLLICLE STIMULATING HORMONE RECEPTOR |
| U05875 | INTERFERON-GAMMA RECEPTOR BETA CHAIN [interferon gamma receptor accessory factor-1 (AF-1)] |
| U15979; | DELTA-LIKE PROTEIN PRECURSOR (CONTAINS: FETAL ANTIGEN 1) (FA1) (DLK) + |
| [Z12172] | ADRENAL SPECIFIC 30kd PROTEIN GB: X17544 |
| X03541 | HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRK1 TRANSFORMING TYROSINE KINASE PROTEIN) (P140-TRKA) + trk-T3 (P68 TRK-T3 ONCOPROTEIN) |
| X15218 | SKI ONCOGENE |
| X15219 | SKI-RELATED ONCOGENE SNON |
| X74979 | TYROSINE-PROTEIN KINASE CAK [EDDR1; TRK E] |
| A06925 | RELAXIN H2 |
| D10232 | RENIN-BINDING PROTEIN |
| M13981 | INHIBIN ALPHA CHAIN |
| M31159; | IGFBP3 (GROWTH HORMONE-DEPENDENT INSULIN-LIKE GROWTH FACTOR-BINDING PROTEIN) |
| [M35878] | |
| U06863 | FOLLISTATIN-RELATED PROTEIN |
| S85655 | PROHIBITIN |

TABLE 8 (CONT)

| GenBank # | Gene Name |
|--------------------------|--|
| D38122; | FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL) (APT1LG1) (FASL). |
| [U08137] | |
| L11015 | LYMPHOTOXIN-BETA |
| U57059 | FAS ANTIGEN LIGAND [TNF-related apoptosis inducing ligand TRAIL; Apo-2 ligand] |
| X14454 | INTERFERON REGULATORY FACTOR [Interferon regulatory factor 1] |
| Y09392; | WSL-LR, WSL-S1, WSL-S2 + TRAMP (Apo-3) (DDR3) |
| [U75380; U74611; U83597] | |
| M27544 | INSULIN-LIKE GROWTH FACTOR IA |
| M86528 | NEUROTROPHIN-4 |
| M86528; | NT-4 (NT-5) + NT-6 |
| S41541; | |
| [S41540; | |
| S41522 | |
| U14187 | RECEPTOR TYROSINE KINASE LIGAND LERK-3 (EPLG3) |
| U14188 | RECEPTOR TYROSINE KINASE LIGAND LERK-4 (EPLG4) |
| U32659 | INTERLEUKIN-17 |
| U33635 | HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR [colon carcinoma kinase-4 (CCK4)] |
| U68162 | THROMBOPOIETIN RECEPTOR |
| A25270 | IFN-GAMMA ANTAGONIST CYTOKINE |
| A03911 | NEURITE PROMOTING FACTOR(NEXIN), glia derived |
| D49493 | BONE MORPHOGENETIC PROTEIN 3B |
| D49742; | HGF ACTIVATOR LIKE |
| [S83182] | |
| L17075 | TGF-b superfamily receptor type I (ALK-1) (SRK3) |
| L03840 | FGFR4 |
| L19063 | GDNF |
| L37882 | frizzled |
| L20861 | Wnt-5a |
| M62403 | IGFBP4 |
| M65062 | IGFBP5 |
| M73980 | Notch1 |
| M97016 | BONE MORPHOGENETIC PROTEIN 8 (OSTEOGENIC PROTEIN 2) |
| M99437 | notch group protein (N) |
| U43318 | frizzled 5 |
| X07876 | WNT2 OR IRP |
| A26792 | CNTF, ISOFORM B AND C |
| L42379 | BPGF-1 |
| Z71621 | Wnt-13 |
| M21626 | T CELL RECEPTOR VARIABLE REGION |

TABLE 8 (CONT)

| GenBank # | Gene Name |
|-----------|--|
| M25639 | MIF |
| U82169 | frizzled homolog (FZD3) |
| U83508 | angiopoietin-1 |
| U84401 | smoothened |
| U90875 | cytotoxic ligand TRAIL receptor |
| U95299 | Notch4 |
| X91940 | WNT-8B |
| X97057 | WNT-10B |
| AF003521 | Jagged 2 |
| AF028593 | Jagged 1 |
| U77493 | Notch2 |
| U94352 | manic fringe |
| U94354 | lunatic fringe |
| M27968 | FGF2; HEPARIN-BINDING GROWTH FACTOR 2 PRECURSOR (PROSTATROPIN). (HBGF-2) (BASIC FIBROBLAST GROWTH FACTOR) (BFGF) (PROSTATROPIN) |
| L38518 | sonic hedgehog (SHH) |
| M60314 | BONE MORPHOGENETIC PROTEIN 5 |
| M60315 | BONE MORPHOGENETIC PROTEIN 6 |
| M60316 | BONE MORPHOGENETIC PROTEIN 7 (OSTEOGENIC PROTEIN 1) |
| D13365; | GROWTH INHIBITORY FACTOR (METALLOTHIONEIN-III) (MT-III) |
| [M93311] | |
| U46010 | HGF AGONIST/ANTAGONIST |
| L36034 | SDF1A (pre-B cell stimulating factor homologue) |
| M15530 | BCGF1 (B-cell growth factor) |
| M58051; | FGFR3 (FLG-2) |
| [X58255] | |
| M77227 | COMPETITIVE HEPATOCYTE GROWTH FACTOR ANTAGONIST. AN ALTERNATIVE TRANSCRIPT OF THE HEPATOCYTE GROWTH FACTOR PRECURSOR (SCATTER FACTOR) (SF) (HEPATOPOEITIN A) |
| U24163; | frizzled-related FrzB (Fritz) (frezzled (fre)) |
| [U91903; | |
| U68057] | |
| U28811; | CYSTEINE-RICH FIBROBLAST GROWTH FACTOR RECEPTOR [Golgi membrane |
| [U64791] | sialoglycoprotein MG160 (GLG1)] |
| U48801; | VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) + VEGF |
| [U43368] | RELATED FACTOR ISOFORM VRF186 PRECURSOR |
| X02492 | LEUKOCYTE INTERFERON-INDUCIBLE PEPTIDE |
| X85960 | Irk-T3 (P68 TRK-T3 ONCOPROTEIN) |
| X14445 | FGF-3; INT-2 PROTO-ONCOGENE PROTEIN PRECURSOR (FIBROBLAST GROWTH FACTOR-3)(HBGF-3). |
| M37825 | FGF-5; FIBROBLAST GROWTH FACTOR-5 PRECURSOR (HBGF-5). |

TABLE 8 (CONT)

| GenBank # | Gene Name |
|-----------|--|
| AF022385 | apoptosis-related protein TFAR15 (TFAR15) |
| L20471 | extracellular matrix metalloproteinase inducer EMMPRIN |
| M57730 | EPHRIIN-A1 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 1) |
| M37476 | (LERK-1) (IMMEDIATE EARLY RESPONSE PROTEIN B61) (TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 4). |
| U07695 | EPHRIIN TYPE-B RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR HTK). |
| U09304 | EPHRIIN-B1 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 2) (LERK-2) (ELK LIGAND PRECURSOR) (ELK-L). |
| U82938 | CD27BP (Siva) |
| U26403 | EPHRIIN-A5 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 7) (LERK-7) (AL-1). |
| U66406 | EPHRIIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 8) (LERK-8) (EPH-RELATED RECEPTOR TRANSMEMBRANE LIGAND ELK-L3). |
| X95425 | EPHRIIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-1) (EPH HOMOLOGY KINASE-1) (RECEPTOR PROTEIN-TYROSINE KINASE HEK7). |
| M62402 | IGFBP6 |
| AF016268 | death receptor 5 (DR5) |
| AF017986 | secreted apoptosis related protein 1 |
| AF017988 | secreted apoptosis related protein 3 (SARP3) |
| L38734 | EPHRIIN-B2 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 5) (LERK-5) (HTK LIGAND) (HTK-L). |
| M63099 | INTERLEUKIN 1 RECEPTOR ANTAGONIST |
| L40636 | EPHRIIN TYPE-B RECEPTOR 1 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EPH-2) (NET). |
| L41939 | EPHRIIN TYPE-B RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN EPH-3) (ORT) |
| M16591 | TYROSINE-PROTEIN KINASE HCK (EC 2.7.1.112) (P59-HCK AND P60-HCK) (HEMOPOIETIC CELL KINASE). |
| M59371 | EPHRIIN TYPE-A RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ECK) (EPITHELIAL CELL KINASE). |
| M36395 | FGF-9; GLIA-ACTIVATING FACTOR PRECURSOR (GAF) (FIBROBLAST GROWTH FACTOR-9) (HBGF-9). |
| D14838 | BIGH3 |
| M77349 | IGFBP COMPLEX ACID LABILE CHAIN |
| D25216 | FGF-8; ANDROGEN-INDUCED GROWTH FACTOR PRECURSOR (AIGF) (HBGF-8) |
| U36223 | (FIBROBLAST GROWTH FACTOR-8) |
| U41745 | PDGF assoc. protein |
| U43148 | patched homolog (PTC) |
| J02958 | MET |

TABLE 8 (CONT)

| GenBank # | Gene Name |
|-----------|--|
| U66197 | FHF-1 |
| X52599 | BETA NGF |
| X52773 | retinoic acid receptor alpha [RETINOIC ACID RECEPTOR RXR-ALPHA (RXRA)] |
| X63454 | FGF-6; FIBROBLAST GROWTH FACTOR-6 PRECURSOR (HBGF-6) (HST-2). |
| X65923 | FAU |

Cell Cycle Array

In the cell cycle array according to the subject invention, all of the unique polynucleotide probe compositions correspond to genes that are associated with the life cycle of a cell. In a specific cell cycle array of interest, the spots are as provided in Table 9.

TABLE 9

| GenBank # | Gene Name |
|------------------|--|
| Z12020; [M92424] | MDM2 PROTEIN (P53-ASSOCIATED PROTEIN) + MDM2-A (GB: U33199) + MDM2-C (GB: U33201) |
| M14694; [M14695] | p53 |
| U18422 | DP2 (Hump2), dimerization partner of E2F |
| L05624 | DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (EC 2.7.1.-) (MAP KINASE KINASE 1) (MAPKK 1) (ERK ACTIVATOR KINASE 1) (MAPK/ERK KINASE 1) (MEK1). |
| L07540 | ACTIVATOR 1 36 KD SUBUNIT (REPLICATION FACTOR C 36 KD SUBUNIT) (RFC36) |
| L07541 | ACTIVATOR 1 38 KD SUBUNIT (REPLICATION FACTOR C 38 KD SUBUNIT) (RFC38) |
| L20320 | CELL DIVISION PROTEIN KINASE 7 (EC 2.7.1.-) (CDK-ACTIVATING KINASE) (CAK) (39 KD PROTEIN KINASE) (P39 MO15) (STK1) (CAK1). |
| L29511; [M96995] | GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2 ADAPTOR PROTEIN) (ASH PROTEIN). |
| L33264 | CDC2-RELATED KINASE PISSLRE |
| M63488 | REPLICATION PROTEIN A 70 KD DNA-BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE STRANDED DNA-BINDING PROTEIN) |
| M74524 | HHR6A (YEAST RAD6 HOMOLOG) (UBIQUITIN-CONJUGATING ENZYME) (UBCA) |
| M87338 | ACTIVATOR 1 40 KD SUBUNIT (REPLICATION FACTOR C 40 KD SUBUNIT) (RFC40) |
| M87339 | ACTIVATOR 1 37 KD SUBUNIT (REPLICATION FACTOR C 37 KD SUBUNIT) (RFC37) |
| U09579; [L25610] | CYCLIN-DEPENDENT KINASE INHIBITOR 1 (MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN 6) (MDA-6) (P21) (CDK-INTERACTING PROTEIN 1) (CIP1) (WAF1) (CDKN1A) (CDKN1) (SDI1) (PIC1) (CAP20) |
| M68520 | CELL DIVISION PROTEIN KINASE 2 (EC 2.7.1.-) (P33 PROTEIN KINASE) |
| M81933 | cdc25A; M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) |
| M92287 | CYCLIN D3 |
| M96684 | TRANSCRIPTIONAL ACTIVATOR PROTEIN PUR-ALPHA |
| X51688 | CYCLIN A |
| X03484 | RAF ONCOGENE |
| X59798; [M64349] | CYCLIN D1 (CYCLIN PRAD1) (BCL-1 ONCOGENE) |
| D13639 [M90813] | CYCLIN D2 |
| HT3218 [K00065] | SUPEROXIDE DISMUTASE [Superoxide dismutase 1 (Cu/Zn)] |
| D21235 | UV EXCISION REPAIR PROTEIN PROTEIN RAD23 [xeroderma pigmentosum group C repair complementing protein HHR23A] |
| U11791 [U12685] | CYCLIN H |
| L26318 | STRESS-ACTIVATED PROTEIN KINASE JNK1 (EC 2.7.1.-) (C-JUN N-TERMINAL KINASE 1) (JNK-46) |
| L27211 | CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). (CDKN2A) |

TABLE 9 (CONT)

| GenBank # | Gene Name |
|------------------|--|
| L35253; [L35263] | MITOGEN-ACTIVATED PROTEIN KINASE P38 (EC 2.7.1.1) (MAP KINASE P38) (CYTOKINE SUPPRESSIVE ANTI-INFLAMMATORY DRUG BINDING PROTEIN) (CSAID BINDING PROTEIN) (CSBP) (MAX-INTERACTING PROTEIN 2) (MAP KINASE MXI2). |
| M13228 | N-myc |
| M15400 | Retinoblastoma susceptibility (RB1 retinoblastoma-assoc) |
| M25753 | CYCLIN B1 G2/MITOTIC-SPECIFIC |
| M60974 | GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD45 (DNA-DAMAGE INDUCIBLE TRANSCRIPT 1) (DDIT1). |
| M73812 | CYCLIN E |
| S40706 [S62138] | GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD153 (DNA-DAMAGE INDUCIBLE PROTEIN) (CHOP). |
| U40343; [U20498] | CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D). |
| U47413 [L49504] | CYCLIN G1 |
| U47414 [L49506] | CYCLIN G2 |
| X60188 | EXTRACELLULAR SIGNAL-REGULATED KINASE 1 (EC 2.7.1.1) (ERK1) (INSULIN-STIMULATED MAP2 KINASE) (MAP KINASE 1) (MAPK 1) (P44-ERK1) (ERT2) (P44-MAPK) (MICROTUBULE-ASSOCIATED PROTEIN-2 KINASE). |
| X80692 | EXTRACELLULAR SIGNAL-REGULATED KINASE 3 (EC 2.7.1.1) (ERK3) (MAP KINASE ISOFORM P97) (P97-MAPK). |
| L31951 | STRESS-ACTIVATED PROTEIN KINASE JNK2 (EC 2.7.1.1) (C-JUN N-TERMINAL KINASE 2) (JNK-55). |
| U34819; [U07620] | STRESS-ACTIVATED PROTEIN KINASE JNK3 (EC 2.7.1.1) (C-JUN N-TERMINAL KINASE 3) (JNK3) (MAP KINASE P49 3F12). |
| L29216 | CLK-2 |
| L29220 | CLK-3 |
| L29222 | CLK-1 |
| U10564 | WEE1-LIKE PROTEIN KINASE (EC 2.7.1.12) (Wee1Hu) |
| U22398 | CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITOR P57) (P57KIP2) |
| U33841 | ATAXIA TELANGIECTASIA (ATM) |
| U39657 | DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 6 (EC 2.7.1.1) (MAP KINASE KINASE 6) (MAPKK 6) (MAPK/ERK KINASE 6) (SAPKK3) |
| M81934; [S78187] | cdc25B: M-PHASE INDUCER PHOSPHATASE 2 (EC 3.1.3.48). [CDC25Hu2] |
| U17075; [L36844] | CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B) (MULTIPLE TUMOR SUPPRESSOR 2) (MTS2) [CDKN2B]. |
| X74262 | RBA/p48 |
| X85133 | RBQ1 retinoblastoma binding protein |
| X85753 | CELL DIVISION PROTEIN KINASE 8 (EC 2.7.1.1) (PROTEIN KINASE K35). |

TABLE 9 (CONT)

| GenBank # | Gene Name |
|------------------|--|
| L13698 | GROWTH-ARREST-SPECIFIC PROTEIN 1 (GAS-1). |
| D63878 | NEDD5 PROTEIN HOMOLOG. |
| L23959 | E2F-related transcription factor (DP-1) |
| L25676 | SERINE/THREONINE PROTEIN KINASE PITALRE |
| M14505 | CELL DIVISION PROTEIN KINASE 4 (EC 2.7.1.-) (PSK-J3) |
| M29039 | jun B TRANSACTIVATOR |
| M34065 | cdc25C; M-PHASE INDUCER PHOSPHATASE 3 (EC 3.1.3.48). |
| M35543; [M57298] | cdc42 homolog (G25K) [brain isoform + placental isoform] |
| L22005 | UBIQUITIN-CONJUGATING ENZYME E2-CDC34 |
| M95712 | ral/b- |
| S72008 | CDC10 PROTEIN HOMOLOG |
| U15642 | E2F-5 |
| U24152 | SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA (EC 2.7.1.-) (P65-PAK) (P21- ACTIVATED KINASE) (ALPHA-PAK) |
| U24153 | p21-activated protein kinase (Pak2) |
| U25278 | EXTRACELLULAR SIGNAL-REGULATED KINASE 5 (EC 2.7.1.-) (ERK5) (ERK4) (BMK1 KINASE) |
| U34051 | CYCLIN-DEPENDENT KINASE 5 ACTIVATOR ISOFORM P39I PRECURSOR (CDK5 ACTIVATOR) (P39I). |
| U53442 | MITOGEN-ACTIVATED PROTEIN KINASE P38 BETA (EC 2.7.1.-) (MAP KINASE P38 BETA) |
| L34075 | FKBP-RAPAMYSLIN ASSOCIATED PROTEIN (FRAP) |
| X05360 | CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.-) (P34 PROTEIN KINASE) (CYCLIN-DEPENDENT KINASE 1) (CDK1) |
| L40027 | glycogen synthase kinase 3 |
| X59727 | EXTRACELLULAR SIGNAL-REGULATED KINASE 4 (EC 2.7.1.-) (ERK4) (MAP KINASE ISOFORM P63) (P63-MAPK). |
| X66360 | SERINE/THREONINE-PROTEIN KINASE PCTAIRE-2 |
| X66362 | SERINE/THREONINE-PROTEIN KINASE PCTAIRE-3 |
| X66363 | SERINE/THREONINE-PROTEIN KINASE PCTAIRE-1 |
| X66364 | CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE). |
| X66365 | CELL DIVISION PROTEIN KINASE 6 (EC 2.7.1.-) (KINASE PLSTIRE) |
| X74594 | RB2/p130 |
| X79483 | EXTRACELLULAR SIGNAL-REGULATED KINASE 6 (EC 2.7.1.-) (ERK6) (ERK5) |

TABLE 9 (CONT)

| | GenBank # | Gene Name |
|--|------------------|--|
| | X80343 | CYCLIN-DEPENDENT KINASE 5 ACTIVATOR PRECURSOR (CDK5 ACTIVATOR) (TAU PROTEIN KINASE II 23 KD SUBUNIT) (TPKII REGULATORY SUBUNIT) (P23) (P25) (P35). |
| | X85134 | RBQ-3 |
| | M15796; [J04718] | PCNA (CYCLIN) |
| | AF001954 | growth inhibitor p33ING1 (ING1) |
| | AF007111 | MDM2-like p53-binding protein (MDMX) |
| | D89667 | C-myc binding protein |
| | U66469 | p53-dependent cell growth regulator CGR19 |
| | U77949 | CDC6-RELATED PROTEIN |
| | U78876 | MEK KINASE 3 |
| | Y11416 | p73, a monoallelically expressed p53-related protein |
| | Y10479 | E2F-3 |
| | U02570 | CDC42 GTPase-activating protein |
| | L11285 | DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 2 (EC 2.7.1.-) (MAP KINASE KINASE 2) (MAPKK 2) (ERK ACTIVATOR KINASE 2) (MAPK/ERK KINASE 2) (MEK2). |
| | M63167 | Akt1 (rac protein kinase alpha, protein kinase B, c-Akt) |
| | S57153; S57160 | RBP1(RETINOBLASTOMA-BINDING PROTEIN) |
| | U23435; U31089 | Abl interactor 2 (Abl-2) + Abl binding protein 3 (AblBP3) [ArgBPB] |
| | M29870; [M31467] | RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 (P21-RAC1) (RAS-LIKE PROTEIN TC25) |
| | M96577 | E2F-1 pRB-binding protein |
| | U25265 | DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 5 (EC 2.7.1.-) (MAP KINASE KINASE 5) (MAPKK 5) (MAPK/ERK KINASE 5). |
| | X66357 | CELL DIVISION PROTEIN KINASE 3 (EC 2.7.1.-). |
| | M74091 | CYCLIN C G1/S-SPECIFIC |
| | M80629 | CDC2-RELATED PROTEIN KINASE CHED |
| | S66431 | RBP2 retinoblastoma binding protein |
| | U00001 | CDC27HS PROTEIN |
| | U01038 | SERINE/THREONINE-PROTEIN KINASE PLK (EC 2.7.1.-) (PLK-1) (STPK13) |
| | D50310 | CYCLIN I |
| | U18291 | CDC16HS. |
| | U63131 | CDC37 HOMOLOG. |
| | U69276 | GRB-IR / GRB10 |
| | X66358 | SERINE/THREONINE-PROTEIN KINASE KIALRE |

Other Representative Arrays

In a neuroarray according to the subject invention, all of the unique polynucleotide probe compositions will correspond to genes that are expressed in brain related tissues. Genes that are represented on the array are key genes, by which is meant that they have been reported to play primary roles in a variety of different biological processes in brain tissues. Genes of interest that may be represented on the array include: ion channel/transport proteins; receptors; cell cycle regulators; stress response proteins; apoptosis proteins; signal transduction proteins; transcriptional factors; growth factors/interleukins/hormones; oncogenes and tumor suppressors; cell surface/adhesion proteins; DNA synthesis/repair/recombination genes; and metabolic pathway enzymes.

In certain embodiments, of particular interest is an array having the following types of genes represented on its surface: nuclear proteins; endoplasmic reticulum proteins; golgi complex proteins; endosomal proteins; lysosomal proteins; peroxisomal proteins; mitochondrial proteins; cytoplasmic proteins; cytoskeletal proteins; plasma membrane proteins; post synaptic and dendritic proteins; axonal and nerve terminal proteins; secreted proteins, neuropeptides, hormones and growth factors; extracellular matrix proteins; astrocyte and oligodendroglial proteins; immune system proteins; developmentally regulated proteins; regionally regulated proteins; and disease related proteins.

Other representative arrays include: (1) rat arrays, in which each of the unique polynucleotide corresponds to a key rat gene; (2) blood arrays, in which each unique polynucleotide corresponds to a gene associated cells and tissues associated with the cardiovascular system; (3) rat stress arrays; and (4) mouse stress arrays, in which each unique polynucleotide corresponds to a gene associated with the stress response of murine cells.

METHODS OF USING THE SUBJECT ARRAYS

The subject arrays find use in a variety of different applications in which one is interested in detecting the occurrence of one or more binding events between target nucleic acids and probes on the array and then relating the occurrence of the binding event(s) to the presence of a target(s) in a sample. In general, the device will be contacted with the sample suspected of containing the target under conditions sufficient for binding of any target

present in the sample to a complementary polynucleotide present on the array. Generally, the sample will be a fluid sample and contact will be achieved by introduction of an appropriate volume of the fluid sample onto the array surface, where introduction can be pipette, deposition, and the like.

5

Generation of Labeled Target

Targets may be generated by methods known in the art. mRNA can be labeled and used directly as a target, or converted to a labeled cDNA target. Generally, such methods include the use of oligonucleotide primers. Primers that may be employed include oligo dT,
10 random primers, e.g. random hexamers and gene specific primers.

Of particular interest in the generation of labeled target is the use of a set of a representational number of gene specific primers, as described in U.S. Patent Application No. 08/ 859,998, the disclosure of which is herein incorporated by reference. As the subject sets comprise a representational number of primers, the total number of different primers in
15 any given set will be only a fraction of the total number of different or distinct RNAs in the sample, where the total number of primers in the set will generally not exceed 80 %, usually will not exceed 50 % and more usually will not 20% of the total number of distinct RNAs, usually the total number of distinct messenger RNAs (mRNAs), in the sample. Any two given RNAs in a sample will be considered distinct or different if they comprise a stretch of
20 at least 100 nucleotides in length in which the sequence similarity is less than 98%, as measured using the FASTA algorithm at default settings. As the sets of gene specific primers comprise only a representational number of primers, with physiological sources comprising from 5,000 to 50,000 distinct RNAs, the number of different gene specific primers in the set of gene specific primers will typically range from about 20 to 10,000, usually from 50 to
25 2,000 and more usually from 75 to 1500.

Each of the gene specific primers of the sets described above will be of sufficient length to specifically hybridize to a distinct nucleic acid member of the sample, e.g. RNA or c DNA, where the length of the gene specific primers will usually be at least 8 nt, more usually at least 20 nt and may be as long as 25 nt or longer, but will usually not exceed 50 nt.
30 The gene specific primers will be sufficiently specific to hybridize to complementary template sequence during the generation of labeled nucleic acids under conditions sufficient for first strand cDNA synthesis, which conditions are known by those of skill in the art. The

number of mismatches between the gene specific primer sequences and their complementary template sequences to which they hybridize during the generation of labeled nucleic acids in the subject methods will generally not exceed 20 number %, usually will not exceed 10 number % and more usually will not exceed 5 number %.

5 Generally, the sets of gene specific primers will comprise primers that correspond to at least 20, usually at least 50 and more usually at least 75 distinct genes as represented by distinct mRNAs in the sample, where the term "distinct" when used to describe genes is as defined above, where any two genes are considered distinct if they comprise a stretch of at least 100 nt in their RNA coding regions in which the sequence similarity does not exceed
10 98%, as determined using the FASTA algorithm at default settings.

 The gene specific oligonucleotide primers may be synthesized by conventional oligonucleotide chemistry methods, where the nucleotide units may be: (a) solely nucleotides comprising the heterocyclic nitrogenous bases found in naturally occurring DNA and RNA, *e.g.* adenine, cytosine, guanine, thymine and uracil; (b) solely nucleotide analogs which are
15 capable of base pairing under hybridization conditions in the course of DNA synthesis such that they function as the above nucleotides found in naturally occurring DNA and RNA, where illustrative nucleotide analogs include inosine, xanthine, hypoxanthine, 1,2-diaminopurine and the like; or (c) from combinations of the nucleotides of (a) and nucleotide analogs of (b), where with primers comprising a combination of nucleotides and analogues
20 thereof, the number of nucleotide analogues in the primers will typically be less than 25 and more typically less than 5. The gene specific primers may comprise reporter or hapten groups, usually 1 to 2, which serve to improve hybridization properties and simplify detection procedure.

 Depending on the particular point at which the gene specific primers are employed in
25 the generation of the labeled nucleic acids, *e.g.* during first strand cDNA synthesis or following one or more distinct amplification steps, each gene specific primer may correspond to a particular RNA by being complementary or similar, where similar usually means identical, to the particular RNA. For example, where the gene specific primers are employed in the synthesis of first strand cDNA, the gene specific primers will be
30 complementary to regions of the RNAs to which they correspond.

 Each gene specific primer can be complementary to a sequence of nucleotides which is unique in the population of nucleic acids, *e.g.* mRNAs, with which the primers are

contacted, or one or more of the gene specific primers in the set may be complementary to several nucleic acids in a given population, *e.g.* multiple mRNAs, such that the gene specific primer generates labeled nucleic acid when one or more of set of related nucleic acid species, *e.g.* species having a conserved region to which the primer corresponds, are present in the sample. Examples of such related nucleic acid species include those comprising: repetitive sequences, such as Alu repeats, A1 repeats and the like; homologous sequences in related members of a gene-family; polyadenylation signals; splicing signals; or arbitrary but conserved sequences.

Depending on the particular nature of the labeled nucleic acid generation step of the subject methods, the gene specific primers may be modified in a variety of ways. One way the gene specific primers may be modified is to include an anchor sequence of nucleotides, where the anchor is usually located 5' of the gene specific portion of the primer and ranges in length from 10 to 50 nt in length, usually 15 to 40 nt in length. The anchor sequence may comprise a sequence of bases which serves a variety of functions, such as a sequence of bases which correspond to the sequence found in promoters for bacteriophage RNA polymerase, *e.g.* T7 polymerase, T3 polymerase, SP6 polymerase, and the like; arbitrary sequences which can serve as subsequent primer binding sites; and the like.

Turning now to the methods employing the above sets of gene specific primers, the first step in the subject methods is to obtain a sample of nucleic acids, usually RNAs, from a physiological source, usually a plurality of physiological sources, where the term plurality is used to refer to 2 or more distinct physiological sources. The physiological source of RNAs will typically be eukaryotic, with physiological sources of interest including sources derived from single celled organisms such as yeast and multicellular organisms, including plants and animals, particularly mammals, where the physiological sources from multicellular organisms may be derived from particular organs or tissues of the multicellular organism, or from isolated cells derived therefrom. Thus, the physiological sources may be different cells from different organisms of the same species, *e.g.* cells derived from different humans, or cells derived from the same human (or identical twins) such that the cells share a common genome, where such cells will usually be from different tissue types, including normal and diseased tissue types, *e.g.* neoplastic, cell types. In obtaining the sample of RNAs to be analyzed from the physiological source from which it is derived, the physiological source may be subjected to a number of different processing steps, where such processing steps

might include tissue homogenation, nucleic acid extraction and the like, where such processing steps are known to those of skill in the art. Methods of isolating RNA from cells, tissues, organs or whole organisms are known to those of skill in the art and are described in Maniatis *et al.*, Molecular Cloning: A Laboratory Manual (Cold Spring Harbor Press)(1989).

The next step in the subject methods is the generation of labeled nucleic acids representative of the nucleic acid, usually RNA, profile of the physiological source. As mentioned above, a set of gene specific primers is used to generate the labeled nucleic acids from the sample of RNAs, where the labeled nucleic acids generated in this step may serve as "target" in subsequent assays in which the differences in the RNA profiles of at least two sources are analyzed. As used herein, the term "target" refers to single stranded RNA, single stranded DNA and double stranded DNA, where the target is generally greater than 50 nt in length.

The set of primers may be used either in first strand cDNA synthesis or following one or more amplification steps. Furthermore, the actual synthesis of the labeled nucleic acids may be at the same step during which the sets of gene specific primers are employed, or the synthesis of the labeled nucleic acids may be one more steps subsequent to the step in which the sets of gene specific primers are employed.

In a first embodiment of the invention, the set of gene specific primers is used to generate labeled first strand cDNA, where the labeled first strand cDNA is representative of the RNA profile of the physiological source being assayed. The labeled first strand cDNA is prepared by contacting the RNA sample with the primer set and requisite reagents under conditions sufficient for reverse transcription of the RNA template in the sample. Requisite reagents contacted with the primers and RNAs are known to those of skill in the art and will generally include at least an enzyme having reverse transcriptase activity and dNTPs in an appropriate buffer medium.

A variety of enzymes, usually DNA polymerases, possessing reverse transcriptase activity can be used for the first strand cDNA synthesis step. Examples of suitable DNA polymerases include the DNA polymerases derived from organisms selected from the group consisting of a thermophilic bacteria and archaeobacteria, retroviruses, yeasts, Neurosporas, Drosophilas, primates and rodents. Preferably, the DNA polymerase will be selected from the group consisting of Moloney murine leukemia virus (M-MLV) as described in United

States Patent No. 4,943,531 and M-MLV reverse transcriptase lacking RNaseH activity as described in United States Patent No. 5,405,776 (the disclosures of which patents are herein incorporated by reference), human T-cell leukemia virus type I (HTLV-I), bovine leukemia virus (BLV), Rous sarcoma virus (RSV), human immunodeficiency virus (HIV) and
5 Thermus aquaticus (Taq) or Thermus thermophilus (Tth) as described in United States Patent No. 5,322,770, the disclosure of which is herein incorporated by reference. Suitable DNA polymerases possessing reverse transcriptase activity may be isolated from an organism, obtained commercially or obtained from cells which express high levels of cloned genes encoding the polymerases by methods known to those of skill in the art, where the
10 particular manner of obtaining the polymerase will be chosen based primarily on factors such as convenience, cost, availability and the like.

The various dNTPs and buffer medium necessary for first strand cDNA synthesis through reverse transcription of the primed RNAs may be purchased commercially from various sources, where such sources include Clontech, Sigma, Life Technologies,
15 Amersham, Boehringer-Mannheim. Buffer mediums suitable for first strand synthesis will usually comprise buffering agents, usually in a concentration ranging from 10 to 100 μ M which typically support a pH in the range 6 to 9, such as Tris-HCl, HEPES-KOH, etc.; salts containing monovalent ions, such as KCl, NaCl, etc., at concentrations ranging from 0-200 mM; salts containing divalent cations like $MgCl_2$, $Mg(OAc)$ etc, at concentrations usually
20 ranging from 1 to 10 mM; and additional reagents such as reducing agents, e.g. DDT, detergents, albumin and the like. The conditions of the reagent mixture will be selected to promote efficient first strand synthesis. Typically the set of primers will first be combined with the RNA sample at an elevated temperature, usually ranging from 50 to 95 $^{\circ}$ C, followed by a reduction in temperature to a range between about 0 to 60 $^{\circ}$ C, to ensure
25 specific annealing of the primers to their corresponding RNAs in the sample. Following this annealing step, the primed RNAs are then combined with dNTPs and reverse transcriptase under conditions sufficient to promote reverse transcription and first strand cDNA synthesis of the primed RNAs. By using appropriate types of reagents, all of the reagents can be combined at once if the activity of the polymerase can be postponed or timed to start after
30 annealing of the primer to the RNA.

In this embodiment, one of either the gene specific primers or dNTPs, preferably the dNTPs, will be labeled such that the synthesized cDNAs are labeled. By labeled is meant

that the entities comprise a member of a signal producing system and are thus detectable, either directly or through combined action with one or more additional members of a signal producing system. Examples of directly detectable labels include isotopic and fluorescent moieties incorporated into, usually covalently bonded to, a nucleotide monomeric unit, *e.g.* dNTP or monomeric unit of the primer. Isotopic moieties or labels of interest include ³²P, ³³P, ³⁵S, ¹²⁵I, and the like. Fluorescent moieties or labels of interest include coumarin and its derivatives, *e.g.* 7-amino-4-methylcoumarin, aminocoumarin, bodipy dyes, such as Bodipy FL, cascade blue, fluorescein and its derivatives, *e.g.* fluorescein isothiocyanate, Oregon green, rhodamine dyes, *e.g.* texas red, tetramethylrhodamine, eosins and erythrosins, cyanine dyes, *e.g.* Cy3 and Cy5, macrocyclic chelates of lanthanide ions, *e.g.* quantum dyeTM, fluorescent energy transfer dyes, such as thiazole orange-ethidium heterodimer, TOTAB, etc. Labels may also be members of a signal producing system that act in concert with one or more additional members of the same system to provide a detectable signal. Illustrative of such labels are members of a specific binding pair, such as ligands, *e.g.* biotin, fluorescein, digoxigenin, antigen, polyvalent cations, chelator groups and the like, where the members specifically bind to additional members of the signal producing system, where the additional members provide a detectable signal either directly or indirectly, *e.g.* antibody conjugated to a fluorescent moiety or an enzymatic moiety capable of converting a substrate to a chromogenic product, *e.g.* alkaline phosphatase conjugate antibody; and the like.

In one preferred embodiment, the member of the signal producing system bound to the nucleotide is functional group capable of covalently binding to additional members of the signal producing system to generate a detectable label. Examples of such functional groups or moieties include amino, sulfhydryl, azido, isothiocyanate, sulfoxyl, and the like. The labeled target generated using such nucleotides will thus include one or more, usually a plurality of, functional moieties. For detection, the functional moieties of the modified nucleotides can be labeled by conjugation of a label to the functional moiety. A variety of suitable labels and methods for their conjugation to functional moieties are known to those of skill in the art. Examples include labeling of amino-modified cDNA by a succinimidyl ester of an appropriate dye, *e.g.* Alexa, Bodipy, or Cy dyes. Alternatively, label can be entrapped or bonded into structures of microscopic-sized particles. These particles can then be conjugated with the functional moieties of the target.

For each sample of RNA, one can generate labeled oligos with the same labels. Alternatively, one can use different labels for each physiological source, which provides for additional assay configuration possibilities, as described in greater detail below.

In a variation of the above embodiment, where desired one can generate labeled RNA
5 instead of labeled first strand cDNA. In this embodiment, first strand cDNA synthesis is carried out in the presence of unlabeled dNTPs and unlabeled gene specific primers. However, the primers are optionally modified to comprise a promotor for an RNA polymerase, such as T7 RNA polymerase, T3 RNA polymerase, SP6 RNA polymerase, and the like. In this embodiment, following first strand cDNA synthesis, the resultant single
10 stranded cDNA is then converted to double stranded cDNA, where the resultant double stranded cDNA comprises the anchor sequence comprising the promoter region. Conversion of the mRNA:cDNA hybrid following first strand synthesis can be carried out as described in Okayama & Berg, *Mol. Cell. Biol.* (1982) 2:161-170, and Gubler & Hoffman, *Gene* (1983) 25: 253-269, where briefly the RNA is digested with a ribonuclease, such as E.coli
15 RNase H, followed by repair synthesis using a DNA polymerase like DNA polymerase I, etc., and E.coli DNA ligase. One may also employ the modification of this basic method described in Wu, R, ed., *Methods in Enzymology* (1987), vol. 153 (Academic Press). Next, the double stranded cDNA is contacted with RNA polymerase and dNTPs, including labeled dNTPs as described above, to produce linearly amplified labeled ribonucleic acids. For
20 cDNA lacking the anchor sequence comprising a promoter region, a polymerase that does not need a promoter region but instead can initiate RNA strand synthesis randomly from cDNA, such as core fragment of E.Coli RNA polymerase, may be employed.

In another embodiment of the subject invention, the labeled nucleic acid generation step comprises one or more enzymatic amplification steps in which multiple DNA copies of
25 the initial RNAs present in the sample are produced, from which multiple copies of the initial RNA or multiple copies of antisense RNA (aRNA) may be produced, using the polymerase chain reaction, as described in U.S. Pat. No. 4,683,195, the disclosure of which is herein incorporated by reference, in which repeated cycles of double stranded DNA denaturation, oligonucleotide primer annealing and DNA polymerase primer extension are
30 performed, where the PCR conditions may be modified as described in U.S. Pat No. 5,436,149, the disclosure of which is herein incorporated by reference.

In one embodiment involving enzymatic amplification, the set of gene-specific primers are employed in the generation of the first strand cDNA, followed by amplification of the first strand cDNA to produce amplified numbers of labeled cDNA. In this embodiment, as a set of gene-specific primers is employed in the first strand synthesis step,
 5 only a representative proportion of the total RNA in the sample is amplified during the subsequent amplification steps.

Amplification of the first strand cDNA can be conveniently achieved by using a CAPswitch™ oligonucleotide as described in U.S. Patent Application Serial No. 08/582,562, the disclosure of which is herein incorporated by reference. Briefly, the CAPswitch™
 10 technology uses a unique CAPswitch™ oligonucleotide in the first strand cDNA synthesis followed by PCR amplification in the second step to generate a high yield of ds cDNA. When included in the first-strand cDNA synthesis reaction mixture, the CAPswitch™ oligonucleotide serves as a short extended template. When reverse transcriptase stops at the
 15 5' end of the mRNA template in the course of first strand cDNA synthesis it switches templates and continues DNA synthesis to the end of the CAPswitch™ oligonucleotide. The resulting ss cDNA incorporates at the 3' end, sequence which is complimentary to complete 5' end of the mRNA and the CAPswitch™ oligonucleotide sequence.

Of particular interest as the CAPswitch™ oligonucleotide are oligonucleotides having the following formula:

20



wherein:

dN represents a deoxyribonucleotide selected from among dAMP, dCMP, dGMP and
 25 dTMP;

m represents an integer 0 and above, preferably from 10 to 50;

rN represents a ribonucleotide selected from the group consisting of AMP, CMP, GMP and UMP, preferably GMP; and

n represents an integer 0 and above, preferably from 3 to 7.

30

The structure of the CAPswitch™ oligonucleotide may be modified in a number of ways, such as by replacement of 1 to 10 nucleotides with nucleotide analogs, incorporation

of terminator nucleotides, such as 3'-amino NMP, 3'-phosphate NMP and the like, or non-natural nucleotides which can improve efficiency of the template switching reaction but still retain the main function of the CAPswitch™ oligonucleotide *i.e.* CAP-dependent extension of full-length cDNA by reverse transcriptase using CAPswitch™ oligonucleotide as a template.

In using the CAPswitch™ oligonucleotide, first strand cDNA synthesis is carried out in the presence of a set of gene specific primers and a CAPswitch™ oligonucleotide, where the gene specific primers have been modified to comprise an arbitrary anchor sequence at their 5' ends. The first strand cDNA is then combined with primer sequences complementary to: (a) all or a portion of the CAPswitch™ oligonucleotide and (b) the arbitrary anchor sequence of the gene specific primers and additional PCR reagents, such as dNTPs, DNA polymerase, and the like, under conditions sufficient to amplify the first strand cDNA. Conveniently, PCR is carried out in the presence of labeled dNTPs such that the resultant, amplified cDNA is labeled and serves as the labeled or target nucleic acid. Labeled nucleic acid can also be produced by carrying out PCR in the presence of labeled primers, where either or both the CAPswitch™ oligonucleotide complementary primer and anchor sequence complementary primer may be labeled. In yet an alternative embodiment, instead of producing labeled amplified cDNA, one may generate labeled RNA from the amplified ds cDNA, *e.g.* by using an RNA polymerase such as E.coli RNA polymerase, or other RNA polymerases requiring promoter sequences, where such sequences may be incorporated into the arbitrary anchor sequence.

Instead of using the set of gene specific primers in the first strand cDNA synthesis step followed by subsequent amplification of only a representative fraction of the total number of distinct RNA species in the sample, one may also amplify all of the RNAs in the sample and use the set of gene specific primers to generate labeled nucleic acid following amplification. This embodiment may find use in situations where the RNA of interest to be amplified is known or postulated to be in small amounts in the sample.

In this embodiment, first strand synthesis is carried out using: (a) an oligo dT primer that usually comprises an arbitrary anchor sequence at its 5' end and (b) a CAPswitch™ oligonucleotide. During first strand synthesis the oligo(dT) anneals to the polyA tail of the mRNA in the sample and synthesis extends beyond the 3' end of the RNA to include the CAPswitch™ oligonucleotide, yielding a first strand cDNA comprising an arbitrary

sequence at its 5' end and a region complementary to the CAPswitch™ oligonucleotide at its 3' end. The length of the dT primer will typically range from 15 to 30 nts, while the arbitrary anchor sequence or portion of the primer will typically range from 15 to 25 nt in length.

Following first strand synthesis, the cDNA is amplified by combining the first strand
5 cDNA with primers that correspond at least partially to the anchor sequence and the CAPswitch™ oligonucleotide under conditions sufficient to produce an amplified amount of the cDNA. Labeled nucleic acid is then produced by contacting the resultant amplified cDNA with a set of gene specific primers, a polymerase and dNTPs, where at least one of the gene specific primers and dNTPs are labeled.

10 When employed to generate target, as described above, the gene specific primers of the sets of primers according to the subject invention are typically chosen according to a number of different criteria. In some embodiments of the invention, primers of interest for inclusion in the set include primers corresponding to genes which are typically differentially expressed in different cell types, in disease states, in response to the influence of external
15 agents, factors or infectious agents, and the like. In other embodiments, primers of interest are primers corresponding to genes which are expected to be, or already identified as being, differentially expressed in different cell, tissue or organism types. Preferably, at least 2 different gene functional classes will be represented in the sets of gene specific primers, where the number of different functional classes of genes represented in the primer sets will
20 generally be at least 3, and will usually be at least 5. Gene functional classes of interest include oncogenes; genes encoding tumor suppressors; genes encoding cell cycle regulators; stress response genes; genes encoding ion channel proteins; genes encoding transport proteins; genes encoding intracellular signal transduction modulator and effector factors; apoptosis related genes; DNA synthesis/recombination/repair genes; genes encoding
25 transcription factors; genes encoding DNA-binding proteins; genes encoding receptors, including receptors for growth factors, chemokines, interleukins, interferons, hormones, neurotransmitters, cell surface antigens, cell adhesion molecules *etc.*; genes encoding cell-cell communication proteins, such as growth factors, cytokines, chemokines, interleukins, interferons, hormones *etc.*; and the like. Less preferred are gene specific primers that are
30 subject to formation of strong secondary structures with less than -10kcal/mol; comprise stretches of homopolymeric regions, usually more than 5 identical nucleotides; comprise

more than 3 repetitive sequences; have high, *e.g.* more than 80%, or low, *e.g.* less than 30%, GC content etc.

The particular genes represented in the set of gene specific primers will necessarily depend on the nature of physiological source from which the RNAs to be analyzed are derived. For analysis of RNA profiles of eukaryotic physiological sources, the genes to
5 which the gene specific primers correspond will usually be Class II genes which are transcribed into RNAs having 5' caps, *e.g.* 7-methyl guanosine or 2,2,7-trimethylguanosine, where Class II genes of particular interest are those transcribed into cytoplasmic mRNA comprising a 7-methyl guanosine 5' cap and a polyA tail.

10 For analysis of RNA profiles of mammalian physiological sources, of particular interest are gene specific primers corresponding to the functional gene classes listed above. For analysis of RNA profiles of human physiological sources, the gene specific primers of particular interest are the gene specific primers identified in Table 1 as SEQ ID NO:01 to SEQ ID NO:1372, of U.S. Application Serial No. 08/859,998, the disclosure of which is
15 herein incorporated by reference, where sets of these primers will usually include at least 20 and more usually at least 50 of these specific sequences.

Particular sets of primers of interest in the subject invention are those sets of primers that include primers capable of amplifying at least a portion of the unique polynucleotides present on the arrays with which the target is to be employed. By at least a portion is meant
20 at least about 10, usually at least about 20 and more usually at least about 25 number % (where number is the number of different unique polynucleotides on the array). For examples, sets of primers that include primers capable of amplifying at least a portion of the unique polynucleotides listed in Table 1, *supra*, are of interest. Similarly sets of primers capable of amplifying at least a portion of the unique polynucleotides listed in Tables 2 to 8,
25 *supra*, are also of interest.

In a particularly preferred embodiment, the gene specific primers are preferably those primers that correspond to the different polynucleotide spots on the array that is used in the hybridization assay. Thus, one will preferably employ gene specific primers for each different polynucleotide that is present on the array, so that if the gene is expressed in the
30 particular cell or tissue being analyzed, labeled target will be generated from the sample for that gene. In many embodiments in which the subject arrays are employed, the gene specific primers used to generate the target from the human cell or tissue being analyzed will have

the same sequence as the gene specific primers used to generate the polynucleotide probes present on the array. In this manner, if a particular gene present on the array is expressed in a particular sample, the appropriate target will be generated and subsequently identified. Representative sets of primers falling within this particularly preferred embodiment include:

| 5 | SET | DESCRIPTION |
|---|-----|--|
| | 1 | 1 pair of primers capable of amplifying each polynucleotide listed in Table 1, <i>supra</i> , as well one set of primers capable of amplifying each of the complementary sequences of each of the polynucleotides listed in Table 1. |
| | 2 | 1 pair of primers capable of amplifying each polynucleotide listed in Table 2, <i>supra</i> , as well one set of primers capable of amplifying each of the complementary sequences of each of the polynucleotides listed in Table 2. |
| | 3 | 1 pair of primers capable of amplifying each polynucleotide listed in Table 3, <i>supra</i> , as well one set of primers capable of amplifying each of the complementary sequences of each of the polynucleotides listed in Table 3. |

10 *Hybridization and Detection*

As mentioned above, following preparation of the target nucleic acid from the tissue or cell of interest, the target nucleic acid is then contacted with the array under hybridization conditions, where such conditions can be adjusted, as desired, to provide for an optimum level of specificity in view of the particular assay being performed. Suitable hybridization conditions are well known to those of skill in the art and reviewed in Maniatis et al, *supra* and WO 95/21944. In analyzing the differences in the population of labeled target nucleic acids generated from two or more physiological sources using the arrays described above, each population of labeled target nucleic acids are separately contacted to identical probe arrays or together to the same array under conditions of hybridization, preferably under stringent hybridization conditions (for example, at 50°C or higher and 0.1XSSC (15 mM sodium chloride/0.15 mM sodium citrate)), such that labeled target nucleic acids hybridize to complementary probes on the substrate surface.

Where all of the target sequences comprise the same label, different arrays will be employed for each physiological source (where different could include using the same array at different times). Alternatively, where the labels of the targets are different and

distinguishable for each of the different physiological sources being assayed, the opportunity arises to use the same array at the same time for each of the different target populations. Examples of distinguishable labels are well known in the art and include: two or more different emission wavelength fluorescent dyes, like Cy3 and Cy5, two or more isotopes with different energy of emission, like ^{32}P and ^{33}P , labels which generate signals under different treatment conditions, like temperature, pH, treatment by additional chemical agents, etc., or generate signals at different time points after treatment. Using one or more enzymes for signal generation allows for the use of an even greater variety of distinguishable labels, based on different substrate specificity of enzymes (alkaline phosphatase/peroxidase).

10 Following hybridization, non-hybridized labeled nucleic acid is removed from the support surface, conveniently by washing, generating a pattern of hybridized nucleic acid on the substrate surface. A variety of wash solutions are known to those of skill in the art and may be used.

15 The resultant hybridization patterns of labeled nucleic acids may be visualized or detected in a variety of ways, with the particular manner of detection being chosen based on the particular label of the target nucleic acid, where representative detection means include scintillation counting, autoradiography, fluorescence measurement, colorimetric measurement, light emission measurement and the like.

20 Following detection or visualization, the hybridization patterns may be compared to identify differences between the patterns. Where arrays in which each of the different probes corresponds to a known gene are employed, any discrepancies can be related to a differential expression of a particular gene in the physiological sources being compared.

Utility

25 The subject methods find use in, among other applications, differential gene expression assays. Thus, one may use the subject methods in the differential expression analysis of: (a) diseased and normal tissue, *e.g.* neoplastic and normal tissue, (b) different tissue or tissue types; (c) developmental stage; (d) response to external or internal stimulus; (e) response to treatment; and the like. The subject arrays therefore find use in broad scale expression screening for drug discovery and research, such as the effect of a particular active agent on the expression pattern of genes in a particular cell, where such information can be

30

used to reveal drug toxicity, carcinogenicity, etc., environmental monitoring, disease research and the like.

KITS

5 Also provided are kits for performing analyte binding assays using the subject devices, where kits for carrying out differential gene expression analysis assays are preferred. Such kits according to the subject invention will at least comprise the subject arrays. The kits may further comprise one or more additional reagents employed in the various methods, such as primers for generating target nucleic acids, including a set of gene
10 specific primers according to the subject invention, e.g. primer sets 1 to 9 described above, dNTPs and/or rNTPs, which may be either premixed or separate, one or more uniquely labeled dNTPs and/or rNTPs, such as biotinylated or Cy3 or Cy5 tagged dNTPs, or other post synthesis labeling reagent, such as chemically active derivatives of fluorescent dyes, enzymes, such as reverse transcriptases, DNA polymerases, and the like, various buffer
15 mediums, e.g. hybridization and washing buffers, prefabricated probe arrays, labeled probe purification reagents and components, like spin columns, etc., signal generation and detection reagents, e.g. streptavidin-alkaline phosphatase conjugate, chemifluorescent or chemiluminescent substrate, and the like.

20

The following examples are offered by way of illustration and not by way of limitation.

EXPERIMENTAL

25

Example 1 - Generation of human cDNA array

686 cDNA fragments corresponding 686 different human genes were amplified from quick-clone cDNA (CLONTECH) in 686 separate test tubes using a combination of sense and antisense gene-specific primers: (Set No. 9, described *supra*). Amplification was
30 conducted in a 100- μ l volume containing 2 μ l of mixture of 10 Quick-clone cDNA from placenta, brain, liver, lung, leukocytes, spleen, skeletal muscle, testis, kidney and ovary (CLONTECH), 40 mM Tricine-KOH (pH 9.2 at 22°C), 3.5 mM Mg(OAc)₂, 10 mM KOAc.

75 µg/ml BSA, 200 µM of each dATP, dGTP, dCTP and dTTP, 0.2 µM of each sense and antisense gene-specific primers and 2 µl of KlenTaq Polymerase mix. Temperature parameters of the PCR reactions were as follows: 1 min at 95°C followed by 20-35 cycles of 95°C for 15 sec and 68°C for 2 min; followed by a 10-min final extension at 68°C. PCR products were examined on 1.2% agarose/EtBr gels in 1x TBE buffer. As a DNA size marker a 1 Kb DNA Ladder was used. ds cDNA was then precipitated by addition of a half volume of 4M ammonium acetate (about 35 µl) and 3.7 volumes of 95% ethanol (about 260 µl). After vortexing, the tube was immediately centrifuged at 14,000 r.p.m. in a microcentrifuge for 20 min. The pellet was washed with 80% ethanol without vortexing, centrifuged as above for 10 min, air dried, and dissolved in 10 µl of deionized water. Yield of ds cDNA after the amplification step was about 5 µg. The ds cDNA fragments for all 686 genes were cloned into TA-cloning vector using the manufacturer's recommendations (Invitrogen) and identity of the clones was confirmed by sequence analysis. The ds cDNA inserts with the sequence corresponding 686 genes were amplified by PCR using a combination of antisense and sense gene-specific primers, as described above. The ds cDNA was denatured by adding 1 µl of 10X denaturing solution (1 M NaOH, 10 mM EDTA) and incubating at 65°C for 20 min. All cDNA probes were transferred in 384-well plate and loaded on positively charged nylon membrane (Schleher & Schull) using 384 pin tool and Biomek 2000 (Beckman) robot. The resultant array is described in Table 1.

Example 2 - Generation of ³²P-labeled oligonucleotides during first strand cDNA synthesis

Step A. cDNA synthesis/Labeling Procedure

1 µg of polyA+RNA or total RNA was converted into ³²P-labeled first-strand cDNA as follows. A sufficient volume of master mix for all labeling reactions and 1 extra reaction was prepared as follows to ensure sufficient volume. For each 10-µl labeling reaction, the following reagents were mixed:

| | |
|------|--|
| 2 µl | 5X First-strand buffer (250 µM Tris-HCl pH8.3; 375 mM KCl; 15 mM MgCl ₂) |
| 1 µl | 10XdNTP mix (500 µM dGTP, 500 µM dCTP, 500 µM dTTP, 5 µM dATP) |
| 4 µl | [α- ³² P]dATP (Amersham, 3000 Ci/mmol, 10 mCi/ml) |
| 1 µl | MMLV reverse transcriptase (Amersham, 200 units/µl) |

8 μ l Final volume

Next, the following reagents were combined in a 0.5-ml PCR test tube:

- 1 μ g (1-2 μ l) polyA+RNA sample
- 5 1 μ l 10x gene-specific primers mix (0.2 μ M of each oligonucleotide ID No.
2,4,6,8,10,12,... 1372 from Table 1 of U.S. Patent Application Serial No.
08/859,998, the disclosure of which is herein incorporated by reference.)

- 10 As a control, in separate test tube were mixed 1 μ g of polyA+RNA sample with 1 μ l of oligo
dT primer (CDS1, 5'-d(TCTAGAATTCAGCGCCGC(T)₃₀VN) - 3'
(where V=G or A or C; N=G or A or T or C)

- For each tube, ddH₂O was added to a final volume of 3 μ l and the contents were
- 15 mixed and spun briefly in a microcentrifuge. The tubes were then incubated in a preheated
PCR thermocycler at 70°C for 2 min. The temperature in thermocycle was reduced down to
50°C and the tube contents were incubated for 2 min. 8 μ l of master mix as prepared above
were added to each reaction test tube. The contents of the test tubes were then mixed by
gentle pipetting. The tubes were then incubated in a PCR thermocycler for 20 min at 50°C.
- 20 The reaction was then stopped by adding 1 μ l of 10X termination mix (0.1 M EDTA, 1
mg/ml glycogen).

Step B. Column Chromatography

- The ³²P-labeled cDNAs were separated from unincorporated ³²P-labeled nucleotides
- 25 and small (<0.1- kb) cDNA fragments using the following procedure for each test tube. A
CHROMA SPIN-200 column (CLONTECH, Palo Alto, CA) was placed into a 1.5-ml
microcentrifuge tube, the water was allowed to drain through the column by gravity flow
until the surface of the gel beads emerged in the column matrix. The sample was then
applied to the center of the gel bed's flat surface and allowed to be fully absorbed into the
resin bed. 25 μ l of ddH₂O were then applied and allowed to completely drain out of the
- 30 column. 200 μ l of ddH₂O were then applied and allowed to completely drain out of the
column until there was no liquid left above the resin bed. The column was then transferred to
a clean 1.5-ml microcentrifuge tube.

To collect the first fraction, 100 μ l of ddH₂O were added to the column and allowed to completely drain out of the column. The second, third and fourth fractions were collected in analogous fashion. The tubes with fractions 1-4 were then placed in scintillation counter empty vials, and Cherenkov counts for each fraction were obtained in the tritium channel.

- 5 The fractions which showed the highest Cerenkov counts were pooled.

Example 3 - Generation of Cy3-labeled hybridization polynucleotide target from polyA+RNA using postsynthesis labelling procedure

- 10 In this procedure for generating labeled cDNA target, polyA+RNA is first converted into cDNA that has primary amino groups which are subsequently coupled with Cy3 succinimide ester. This technology allows for a significant increase (about 10 fold) in activity of labeled polynucleotide target and therefore increases the overall sensitivity of detection of gene expression. The same procedure can be used for labeling two (or more)
- 15 samples of RNA. In this case the cDNA synthesis step was the same for both samples but at the labeling step, each cDNA sample was labeled by different and distinguishable labels, e.g. Cy3 and Cy5, Alexa 532 and Bodipy TR, Fluorescein and tetramethyl rhodamine, etc. Each labeled probe was purified separately by column chromatography and, after normalization, were combined together in equal ratio and hybridized with a cDNA array. After
- 20 hybridization, the detection procedure revealed both dye-labeled hybridized target simultaneously, based on the different spectral characteristics (emission wavelength) of the fluorescent labels.

A. cDNA synthesis

- 25 The 10- μ l reaction described below converted 1 μ g of polyA+RNA into amino-modified first-strand cDNA.

For each cDNA synthesis reaction:

1. Enough master mix for all labeling reactions and 1 extra reaction was prepared to ensure sufficient volume.
- 30 For each 10- μ l labeling reaction, the following reagents were mixed:
- | | |
|-----------|---|
| 2 μ l | 5X First-strand buffer (250 μ M Tris-HCl pH8.3; 375 mM KCl; 15 mM MgCl ₂) |
| 1 μ l | 10XdNTP mix (500 μ M dGTP, 500 μ M dCTP, 500 μ M dATP, 100 μ M dTTP, |

and 100 μ M allylamino dUTP)

1 μ l [α -³²P]dATP (Amersham, 3000 Ci/mmol, 10 mCi/ml)

3 μ l H₂O

1 μ l MMLV reverse transcriptase (Amersham, 200 units/ μ l)

5

8 μ l Final volume

2. The following was combined in a 0.5-ml PCR test tube:

1 μ g (1-2 μ l) polyA+RNA sample

- 10 1 μ l 10x gene-specific primers mix (0.2 μ M of each oligonucleotide ID No.
2,4,6,8,10,12,..... 1372) (from Table 1 of U.S. Patent Application No.
08/859,998, the disclosure of which is herein incorporated by reference.)

As a control in separate test tube 1 μ g of polyA+RNA sample was mixed with 1 μ l
15 of oligo dT primer (SEQ ID NO. 1373 from Table 1 of U.S. Application No. 08/859,998).

3. ddH₂O was added to a final volume of 3 μ l.
4. The contents were mixed and the tubes were spun briefly in a microcentrifuge.
5. The tubes were incubated in preheated PCR thermocycler at 70°C for 2 min.
- 20 6. The temperature in the thermocycle was reduced down to 50°C and incubate for 2 min.
7. 8 μ l of master mix were added to each reaction test tube.
8. The contents of the test tubes were mixed by gentle pipeting.
9. The tubes were incubated in a PCR thermocycler for 30 min at 50°C.
- 25 10. The reaction was stopped by increasing temperature up to 70°C for 5 min, then cooled to 37°C.
11. 1 μ l of RNase H (10 units/ μ l) was added and the tubes were incubated at 37°C for 15 min.
12. The reaction was stopped by adding 40 μ l of termination mix (0.3 M sodium acetate, pH 5.0, 1 mM EDTA).
- 30 13. An equal volume (50 μ l) of phenol/chlorophorm/isoamyl alcohol mix (1: 1: 1/24 v/v) was added and extraction was performed. Phases were separated by centrifugation at 14,000 rpm for 10 min.

14. Upper water phase was collected and cDNA was precipitated by adding 2.5 volumes (about 120 μ l) of ethanol.
15. The precipitate was collected by centrifugation at 14,000 rpm for 10 min, the supernatant removed and the precipitate was washed with 80% ethanol.
- 5 16. The precipitate was air dried and dissolved in 10 μ l of 0.1 M sodium bicarbonate buffer, pH 9.0.

Step B. Post synthesis labeling procedure.

1. 1 mg of Cy3 succinimide ester was dissolved in 10 μ l of dimethyl sulfoxide and 10
10 μ l of amino-modified cDNA generated at step 16 was added to it.
2. The mixture was incubated at room temperature overnight.

Step C. Column Chromatography

To purify the Cy3-labeled cDNAs from the unconjugated label, the following was
15 performed for each test tube:

1. CHROMA SPIN-200 column (CLONTECH) was removed from refrigerator and allowed to warm at room temperature for about 1 hour. The column was inverted several times to completely resuspend the gel matrix. (Note: Check for air bubbles in the column matrix. If bubbles are visible, resuspend the matrix in the in the column
20 buffer (ddH₂O) by inverting the column again).
2. The bottom cap from the column was removed, and then the top cap was slowly removed.
3. The column was placed into a 1.5-ml microcentrifuge tube.
4. The water was allowed to drain through the column by gravity flow until the surfaces
25 of the gel beads in the column matrix were visible. (The top of the column matrix should be at the 0.75-ml mark on the wall of the column. If the column contains much less matrix, adjust the volume of the matrix to 0.75ml mark using matrix from another column.)
5. The collected water was discarded.
- 30 6. The sample was applied to the center of the gel bed's flat surface and allowed to be fully absorbed into the resin bed. Care was taken not allow any sample to flow along the inner wall of the column.

7. 25 μ l of ddH₂O were applied and allowed to completely drain out of the column.
8. Apply 200 μ l of ddH₂O and allow the buffer to completely drain out of the column until there was no liquid left above the resin bed.
9. The column was transferred to a clean 1.5-ml microcentrifuge tube.
- 5 10. 100 μ l of ddH₂O were added to the column and allowed to completely drain out of the column.
11. The second, third and fourth fractions were collected by repeating steps 9-10.
12. Cherenkov counts were obtained for each fraction by counting the entire sample in the tritium channel.
- 10 13. The fractions (usually fractions 2-3) which showed highest Cerenkov counts were pooled. Waste column and the fractions (usually fraction 1 and 4) which showed less than 10% counts from peak fractions.

Example 4 - Hybridization ³²P-labeled cDNA Target with cDNA Array

15

A solution of ExpressHyb™ (CLONTECH) and sheared salmon testes DNA (Sigma) was prepared by prewarming 15 ml of ExpressHyb™ at 50-60°C, heating 1.5 mg of sheared salmon testes DNA at 95-100°C for 5 min followed by chilling quickly on ice, and combining the resultant heat-denatured sheared salmon testes DNA with the prewarmed

20 ExpressHyb™.

A cDNA Array as produced in Example 1 above was then placed in a hybridization bottle and 10 ml of the solution prepared above was added to the bottle. Prehybridization was performed for 30 min with continuous agitation at 72°C. Labeled cDNA probe (Example 1, about 200 μ l, total about 2.5×10^6 cpm) with 1/10th of the total volume (about

25 22 μ l) of 10x denaturing solution (1 M NaOH, 10 mM EDTA) was mixed and incubated at 65°C for 20 min. 5 μ l (1 μ g/ μ l) of human Cot-1 DNA was then added, and an equal volume (about 225 μ l) of 2x Neutralizing solution (1M NaHPO₄, pH 7.0) was added and incubation continued at 65°C for 10 min. The mixtures were then combined and thoroughly mixed.

The prehybridization solution was replaced with the solution comprising the labeled

30 oligonucleotide as prepared above and allowed to hybridize overnight with continuous agitation at 65°C. Following hybridization, the hybridization solution was carefully removed

and discarded, replaced with 200 ml of Wash Solution 1 (2X SSC, 1% SDS). The array was washed for 20 min with continuous agitation at 65°C. Washing was repeated four times.

Two additional 20-min washes were then performed in 200 ml of prewarmed Wash Solution 2 (0.1X SSC, 0.5% SDS) with continuous agitation at 65°C. Using forceps, the
5 cDNA array was removed from the container and excess wash solution was removed by shaking.

The damp membrane was immediately wrapped in plastic wrap, mounted on Whatman paper (3mm Chr) and exposed to x-ray film at -70°C with an intensifying screen.

10 Example 5 - Comparison Between Using Sets of Gene Specific Primers and oligo dT

³²P-labeled cDNA target were synthesized by M-MLV reverse transcriptase from a mixture 588 antisense gene-specific primers (B) or oligo dT(A) using placenta polyA+RNA as a template as described in Example 2. Primer extension products generated by reverse
15 transcription were purified by gel filtration as described in Example 2 and hybridized separately with two cDNA arrays comprising 588 human genes under identical conditions as described in Example 4. Signals which can be detected by using cDNA target generated using the set of gene specific primers but can not be detected by using conventional target generated with oligo dT primers were observed. Note, the level of non-specific background
20 detected as signal generated by membrane alone outside of the regions with immobilized probes generated by target generated using oligo dT primers was significantly higher in comparison with the background generated by the target generated by using the sets of gene specific primers.

25 Example 6 - Generation of cDNA array probe immobilized on glass slides.

50 cDNA fragments corresponding to 50 different human genes were amplified from plasmid clones containing corresponding cDNA fragments in 96 well plates using combination of vector primer ID No. 1376 and ID No. 1377 or sense and antisense gene-specific primers: ID No. 1+2, 3+4,5+6,7+8,.... 100+101 (from Table 1 of U.S. Patent
30 Application No. 08/859,998, the disclosure of which is herein incorporated by reference). Amplification was conducted in a 400-μl volume containing 2 ng of plasmid DNA, 40 mM Tricine-KOH (pH 9.2 at 22°C), 3.5 mM Mg(OAc)₂, 10 mM KOAc, 75 μg/ml BSA, 200 μM

of each dATP, dGTP, dCTP and dTTP, 0.2 μ M of each primers and 2 μ l of KlenTaq Polymerase mix (CLONTECH). Temperature parameters of the PCR reactions were as follows: 1 min at 95°C followed by 30 cycles of 95°C for 15 sec and 68°C for 2 min; followed by a 10-min final extension at 68°C. PCR products were examined on 1.2% agarose/EtBr gels in 1 x TBE buffer. As a DNA size marker, a 1 Kb DNA Ladder was used. ds cDNA was then precipitated by addition of a 10% volume of 3M sodium acetate (pH 5-0) (about 40 μ l) and 2.5 volumes of 96% ethanol (about 1 ml). After vortexing, the tube was immediately centrifuged at 14,000 r.p.m. in a microcentrifuge for 20 min. The pellet was washed with 80% ethanol without vortexing, centrifuged as above for 10 min, air dried, and dissolved in 10 μ l of deionized water. Yield of ds cDNA after amplification step was about 20 μ g. The ds cDNA was solved in 10 μ l of distilled water, 10 μ l of 1 M sodium carbonate buffer, pH 9.5, was added and the ds cDNA was denaturated by heating at 94°C for 5 min and cooled down. The treated glass slides were prepared as following: Glass slides were cleaned overnight in 25% solution of nitric acid at room temperature, washed 3 times by acetone, treated with 1% aminopropyl-trimethoxysilane for 3 hrs at room temperature, washed two times with acetone, heated at 120°C for 6 hrs and then treated with 0.2 % of para-phenylendiisothiocyanate (95:5 acetone-water solution) at room temperature for 3 hrs, then washed two times by acetone and dried in vacuum with desiccant. All cDNA probes were transferred in 384-well plate and printed on treated glass slides using 384 pin tool and Biomek 2000 (Beckman) robot. After printing, the arrays were incubated in wet chamber at 37°C overnight, then ultraviolet-cross linked to the surface by subjecting the slides to 30 mJ of energy (Stratagene Stratalinker). The arrays were washed with 1% of sodium borohydrate in 0.1 M NaOH, then washed 3 times in distilled water, dried in vacuum and stored with desiccant.

Example 7- Hybridization Cy3 -labeled cDNA Target (or Cy3/Cy5 labeled cDNA targets) with glass cDNA array

1. A solution of ExpressHyb (CLONTECH) and sheared salmon testes DNA (Sigma) was prepared as follows:
 - a. 5 ml of ExpressHyb™ was prewarmed at 50-60°C.

- b. 0.5 mg of the sheared salmon testes DNA was heated at 95-100 °C for 5 min, and then chilled quickly on ice.
 - c. Heat-denatured sheared salmon testes DNA was mixed with prewarmed ExpressHyb.
- 5 2. The glass cDNA array was placed in a hybridization container, and 1 ml of the solution prepared in step 1 above was added.
 3. Prehybridization was conducted for 5 min with continuous agitation at 65°C.
 4. Labeled cDNA probe as prepared in example 3, step C13, above, (about 200 μ l) was mixed with 2 μ l (1 μ g/ μ l) of human Cot- I DNA , and denatured at 99°C for 2 min.
 - 10 5. The mixture prepared in Step 4 was added to the hybridization box from Step 3 and the two solutions were mixed together thoroughly. The container was sealed by sealing tape.
 6. Hybridization was allowed to proceed overnight with continuous agitation at 65°C.
 - 15 7. The hybridization solution was carefully removed and discarded in an appropriate container, and replaced with 10 ml of Wash Solution 1 (2X SSC, 0.1% SDS). The array was washed for 10 min with continuous agitation at 65°C. The step was repeated two times.
 8. Additional 10-min washes were performed in 10 ml of Wash Solution 2 (0. 1 X SSC, 0.1% SDS) with continuous agitation at 65°C.
 - 20 9. Using forceps, the cDNA array was removed from the container, briefly washed in 0. 1XSSC and excess buffer was removed from surface by centrifugation in a Beckman CS-6R centrifuge at 2000 rpm.
 10. Glass arrays were scanned using a custom-built laser scanner equipped by green (Cy3 chanel) and red (Cy5 chanel) solid state laser built in UCLA. Images were scanned at a resolution of 20 μ m per pixel.
 - 25

It is evident from the above results and discussion that the subject invention provides a rapid, high throughput means to simply and quickly obtain a broad-scale screening of gene expression in a variety of different samples. Only simple hybridization protocols need be employed with the subject arrays, and signals can be detected using any convenient and readily available detection device. Despite their simplicity, assays conducted with the

30

subject arrays yield a large amount of information regarding the expression of numerous different and important genes in a particular sample at substantially the same time, and thus have use in many different types of applications, including drug discovery and characterization, disease research, and the like.

5

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. The citation of any publication is for its disclosure prior to the filing date and should not be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention.

10

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it is readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

15

WHAT IS CLAIMED IS:

1. An array comprising a plurality of polynucleotide spots stably associated with the surface of a solid support, wherein a portion of said plurality of polynucleotide spots comprise a polynucleotide probe composition made up of unique polynucleotides and all of the unique polynucleotides on said array correspond to genes of a specific type.
5
2. The array according to Claim 1, wherein said polynucleotides of said array have an average length of from about 120 to 1000 nt.
- 10 3. The array according to Claims 1 or 2, wherein each of said unique polynucleotides does not cross hybridize with the polynucleotides of any other polynucleotide probe composition on the array.
4. The array according to Claims 1, 2 or 3, wherein said polynucleotide probe
15 composition comprises a population of single stranded identical polynucleotides.
5. The array according to Claims 1, 2 or 3, wherein said polynucleotide probe composition comprises a population of two different complementary single stranded polynucleotides.
20
6. The array according to any of the preceding claims, wherein the density of spots on said array does not exceed about 500/cm².
7. The array according to any of the preceding claims, wherein the number of spots on
25 said array ranges from about 50 to 1000.
8. The array according to any of the preceding claims, wherein said array is selected from the group consisting of a human array, a mouse array, a cancer array, an apoptosis array, a human stress array, an oncogene/tumor suppressor array, a cell-cell interaction array, a cytokine and cytokine receptor array, a rat array, a blood array, a mouse stress array, and a
30 neuroarray.

9. The array according to any of the preceding claims, wherein said solid support is flexible.
10. The array according to any of the preceding claims, wherein said solid support is rigid.
11. The array according to any of the preceding claims, wherein said polynucleotide probes of said array are those listed in a table selected from the group consisting of: Table 1, Table 2, Table 3, Table 4, Table 5, Table 6, Table 7 and Table 8.
12. A method of preparing an array according to any of the preceding claims, said method comprising:
enzymatically generating said unique polynucleotides; and
stably associating said enzymatically-generated, complementary, unique polynucleotides on the surface of said solid support.
13. A set of a representative number of distinct gene specific primers comprising gene specific primers corresponding to at least twenty distinct genes.
14. The set of gene specific primers according to Claim 13, wherein at least two of the twenty distinct genes are from different gene functional classes.
15. The set of gene specific primers according to Claim 14, wherein the set comprises from 20 to 10,000 gene specific primers.
16. The set of gene specific primers according to Claims 13, 14 or 15, wherein the set comprises primers capable of amplifying at least a portion of the polynucleotides present on an array according to any of Claims 1 to 11.
17. The set of gene specific primers according to Claim 16, wherein the set comprises primers capable of amplifying at least 20 of the polynucleotides present on an array according to any of Claims 1 to 11.

18. A method for detecting expression of a gene using a hybridization assay, said method comprising:

contacting at least one labeled target polynucleotide sample with an array according to any of Claims 1 to 11 under hybridization conditions sufficient to produce a hybridization

5 pattern; and

detecting said hybridization pattern.

19. The method according to Claim 18, wherein said method further comprises washing said array prior to said detecting step.

10

20. The method according to Claims 18 or 19, wherein said method further comprises preparing said labeled target polynucleotide sample.

21. The method according to Claim 20, wherein said preparation comprises:

15

obtaining a sample of nucleic acids from a physiological source; and

generating a population of labeled nucleic acids from the nucleic acids sample by

using a set of a representative number of distinct gene specific primers according to any of Claims 13 to 17;

whereby said labeled target polynucleotide sample is produced.

20

22. The method according to Claims 20 or 21, wherein said preparing comprises conjugating a detectable label to a functionalized target polynucleotide.

23. The method according to any of Claims 18 to 22, where said method further

25 comprises:

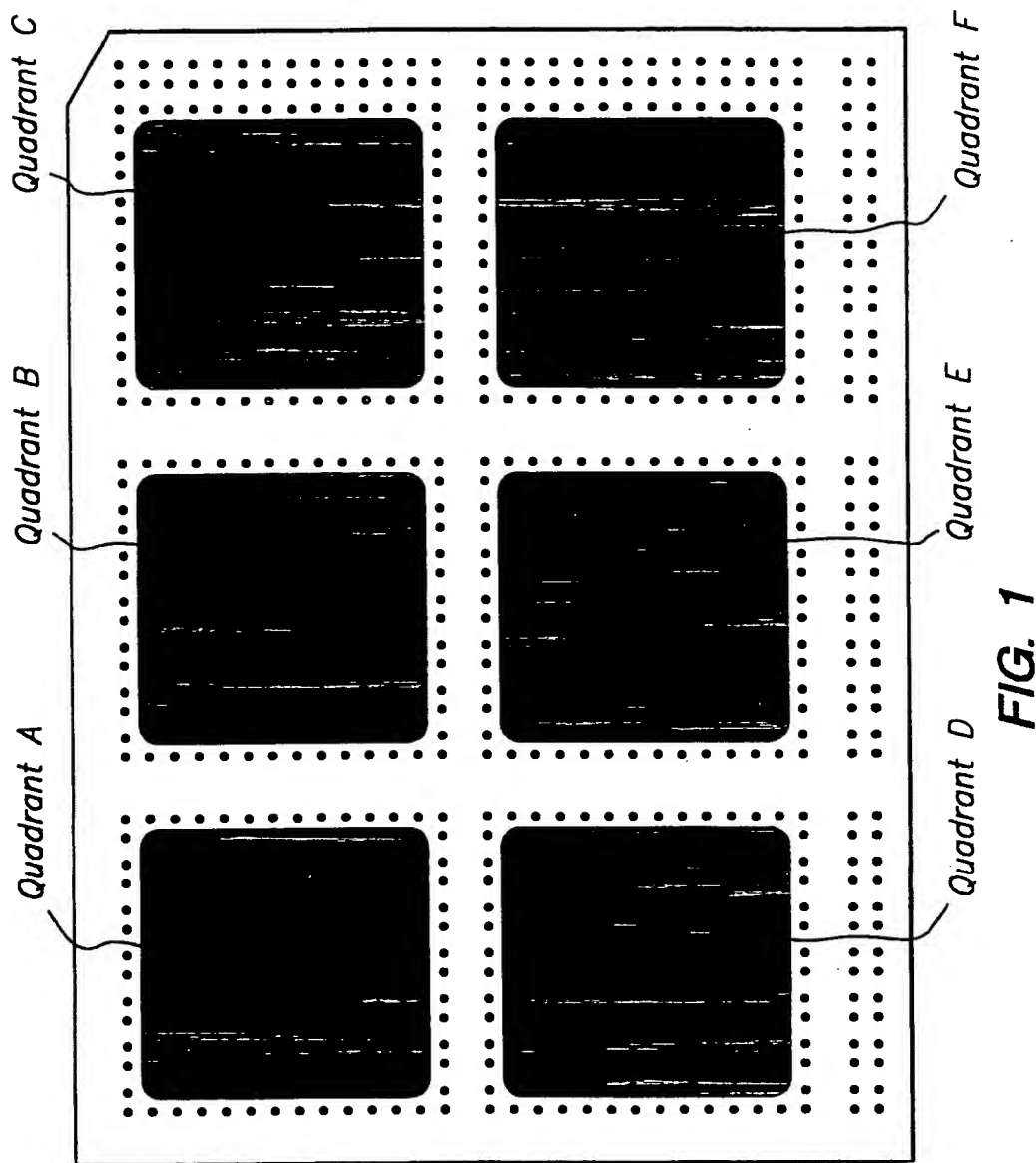
generating a second hybridization pattern; and

comparing said hybridization patterns.

24. The method according to Claim 23, wherein said hybridization patterns are generated

30 on the same array.

25. The method according to Claim 23, wherein the second hybridization patterns are generated on different arrays.
26. A kit for use in a hybridization assay, said kit comprising:
5 an array according to any of Claims 1 to 11.
27. The kit according to Claim 26, wherein said kit further comprises reagents for generating a labeled target polynucleotide sample.
- 10 28. The kit according to Claims 27, wherein said reagents comprise a set of a representational number of gene specific primers according to any of Claims 13 to 17.
29. A kit for use in detecting the differential expression of genes of a plurality of physiological sources, the kit comprising:
15 a set of a representative number of distinct gene specific primers according to any of Claims 13 to 17.



INTERNATIONAL SEARCH REPORT

International application No.

PCT/US98/10561

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : C12Q 1/68; C12P 19/34; C07H 21/02, 21/04

US CL : 435/6, 91.1, 91.2; 536/23.1, 24.3, 24.31, 24.32, 24.33, 24.5

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 91.1, 91.2; 536/23.1, 24.3, 24.31, 24.32, 24.33, 24.5

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|-----------|--|-----------------------|
| Y | EHLERS et al. Differentiation of T cell lymphokine gene expression: The in vitro acquisition of T cell memory. J. Experimental Medicine. January 1991, Vol. 173, pages 25-36, see entire document. | 1-3, 13-15 |
| Y | CHALIFOUR et al. A method for analysis of gene expression patterns. Analytical Biochemistry. 1994, Vol. 216, pages 299-304, see entire document. | 1-3, 13-15 |
| Y | ZHAO et al. High-density cDNA filter analysis: a novel approach for large-scale, quantitative analysis of gene expression. Gene. 1995, Vol. 156, pages 207-213, see entire document. | 1-3, 13-15 |



Further documents are listed in the continuation of Box C.



See patent family annex.

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|--------------------------------------|---|--------------------------|--|
| * *A* *E* *L* *O* *P* | Special categories of cited documents: document defining the general state of the art which is not considered to be of particular relevance earlier document published on or after the international filing date document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) document referring to an oral disclosure, use, exhibition or other means document published prior to the international filing date but later than the priority date claimed | *T* *X* *Y* *Z* | later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art document member of the same patent family |
|--------------------------------------|---|--------------------------|--|

Date of the actual completion of the international search

24 JUNE 1998

Date of mailing of the international search report

10 AUG 1998

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/10561

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|-----------|--|-----------------------|
| Y | NGUYEN et al. Differential gene expression in the murine thymus assayed by quantitative hybridization of arrayed cDNA clones. Genomics. 1995, Vol. 29, pages 207-216, see entire document. | 1-3, 13-15 |
| Y | Atlas human cDNA expression array I. Clontech. April 1997, pages 4-7, see entire document. | 1-3, 13-15 |
| Y | SCHENA et al. Parallel human genome analysis: Microarray-based expression monitoring of 1000 genes. Proc. Natl. Acad. Sci. October 1996, Vol. 93, pages 10614-10619, see entire document. | 1-3, 13-15 |
| Y | GOODWIN et al. Cloning of the human and murine interleukin 7 receptors: demonstration of a soluble, form and homology to a new receptor superfamily. Cell. 23 March 1990, Vol. 60, pages 941-951, see entire document. | 1-3, 13-15 |
| Y | LEONARD et al. Molecular cloning and expression of cDNAs for the human interleukin-2 receptor. Nature. 18 October 1984, Vol. 311, pages 626-631, see entire document. | 1-3, 13-15 |
| Y | GOODWIN et al. Human interleukin 7: Molecular cloning and growth factor activity on human and murine B-lineage cells. Proc. Natl. Acad. Sci. (USA). January 1989, Vol. 86, pages 302-306, see entire document. | 1-3, 13-15 |
| Y | NISHI et al. Cloning and expression of a novel variant of human interferon gamma cDNA. J. Biochem. 1985, Vol. 97, No. 1, pages 153-159, see entire document. | 1-3, 13-15 |

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US98/10561

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☒ Claims Nos.: 4-12, 16-19
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-29, species of SEQ ID NOs: 1-10

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/10561

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

APS, MEDLINE, BIOSIS, CAPLUS

search terms: array, support, bead, nitrocellulose, nylon, filter, hybridize, anneal, DNA, RNA, gene, nucleic, oligo, polynucleotide, spot, pattern, primer

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack Unity of Invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows:

Each of the sequences found in Tables 1-8.

The species listed above do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, the species lack the same or corresponding special technical features for the following reasons:

Each of the sequences found in Tables 1-8 represents a different nucleic acid species which are not joined by a corresponding technical feature such as encoding a similar protein.

According the Official Gazette Notice in October 1996, "Under the Unity of Invention Standard in an International Application or National Stage Application Filed Under 35 U.S.C. § 371, Up to Ten Nucleotide Sequences Will Be Searched and/or Examined Without Payment of An Additional Fee".